

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 20:36:42 ; Search time 2283.3 Seconds
(without alignments)
1386.917 Million cell updates/sec

Title: US-10-003-035-74

Perfect score: 90

Sequence: 1 atgagagtgaggagaataa.....tggtgagatctgtagtgt 90

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA Main:

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- 3: /cgn2_6/ptodata/2/pna/US07_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Fri Mar 12 10:05:53 2004

us-10-003-035-74.rnnp

TYPE: DNA
ORGANISM: Artificial sequence
FEATURE: OTHER INFORMATION: DNA encoding gpl20 signal peptide
PCT-US02-35112-74

Query Match 100.0%; Score 90; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGAGAGTGAAGGAGAAATATCAGCACCTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 2
US-10-003-035-74
Sequence 74, Application US/10003035
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 22488-712
CURRENT APPLICATION NUMBER: US/10/003,035
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.1
SEQ ID NO 74
LENGTH: 90
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE: OTHER INFORMATION: DNA encoding gpl20 signal peptide
US-10-003-035-74

Query Match 100.0%; Score 90; DB 43; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACCTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
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QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 3
US-10-280-915-74
Sequence 74, Application US/10280915
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: MULTIVALENT VACCINATION USING RECOMBINANT ADENOVIRUS
FILE REFERENCE: 22488-741
CURRENT APPLICATION NUMBER: US/10/280,915
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 10/003,035
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.1
SEQ ID NO 74

Result No.	Score	Match	Length	DB	ID	Description
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2	90	100.0	90	43	US-10-003-035-74	Sequence 74, Appl
3	90	100.0	90	48	US-10-280-915-74	Sequence 74, Appl
4	90	100.0	90	48	US-10-286-332A-74	Sequence 58, Appl
5	90	100.0	119	6	US-08-207-526-58	Sequence 41, Appl
6	90	100.0	486	1	PCT-US02-35112-41	Sequence 41, Appl
7	90	100.0	486	43	US-10-003-035-41	Sequence 41, Appl
8	90	100.0	486	48	US-10-280-915-41	Sequence 41, Appl
9	90	100.0	486	48	US-10-286-332A-41	Sequence 41, Appl
10	90	100.0	564	10	US-08-628-686-66	Sequence 66, Appl
11	90	100.0	615	1	PCT-US02-35112-42	Sequence 42, Appl
12	90	100.0	615	43	US-10-003-035-42	Sequence 42, Appl
13	90	100.0	615	48	US-10-280-915-42	Sequence 42, Appl
14	90	100.0	615	48	US-10-286-332A-42	Sequence 42, Appl
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30	90	100.0	1308	48	US-10-286-332A-36	Sequence 36, Appl
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38	90	100.0	2562	1	PCT-US02-35112-32	Sequence 32, Appl
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ALIGNMENTS

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PCT-US02-35112-74
Sequence 74, Application PC/TUS0235112
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 22488-740
CURRENT APPLICATION NUMBER: PCT/US02/35112
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 10/003,035
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.1
SEQ ID NO 74
LENGTH: 90

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us-10-003-035-74.rnrm

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; LENGTH: 90
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding gpl20 signal peptide
US-10-280-915-74

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Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

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US-10-286-332A-74
; Sequence 74, Application US/10286332A
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: METHOD OF VACCINATION THROUGH SEROTYPE ROTATION
; FILE REFERENCE: 22488-738
; CURRENT APPLICATION NUMBER: US/10/286,332A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
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; TYPE: DNA
; ORGANISM: Artificial sequence
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; OTHER INFORMATION: DNA encoding gpl20 signal peptide
US-10-286-332A-74

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Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 5
US-08-207-526-58
; Sequence 58, Application US/08207526
; GENERAL INFORMATION:
; APPLICANT: Shiver, John W
; APPLICANT: Liu, Margaret A
; APPLICANT: Perry, Helen C
; TITLE OF INVENTION: COORDINATE IN VIVO GENE EXPRESSION
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue, P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America

; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,526
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: 19188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3901
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-207-526-58

Query Match      100.0%; Score 90; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 8.2e-18;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PCT-US02-35112-41
; Sequence 41, Application PC/TUS0235112
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 22488-740
; CURRENT APPLICATION NUMBER: PCT/US02/35112
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
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; SEQ ID NO 41
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; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
PCT-US02-35112-41

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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Fri Mar 12 10:05:53 2004

us-10-003-035-74.rnppm

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; Sequence 41, Application US/10003035
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 22488-712
; CURRENT APPLICATION NUMBER: US/10/003,035
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 41
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-003-035-41
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Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
Db      1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
QY      61 CTCCTGGGATGTTGATGATCTGTAGTGCT 90
Db      61 CTCCTGGGATGTTGATGATCTGTAGTGCT 90
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RESULT 8
US-10-280-915-41
; Sequence 41, Application US/10280915
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: MULTIVALENT VACCINATION USING RECOMBINANT ADENOVIRUS
; FILE REFERENCE: 22488-741
; CURRENT APPLICATION NUMBER: US/10/280,915
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 41
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-280-915-41
Query Match      100.0%; Score 90; DB 48; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
Db      1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
QY      61 CTCCTGGGATGTTGATGATCTGTAGTGCT 90
Db      61 CTCCTGGGATGTTGATGATCTGTAGTGCT 90
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RESULT 9
US-10-286-332A-41
; Sequence 41, Application US/10286332A
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: METHOD OF VACCINATION THROUGH SEROTYPE ROTATION
; FILE REFERENCE: 22488-738
; CURRENT APPLICATION NUMBER: US/10/286,332A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 41
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-286-332A-41
Query Match      100.0%; Score 90; DB 48; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
Db      1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
QY      61 CTCCTGGGATGTTGATGATCTGTAGTGCT 90
Db      61 CTCCTGGGATGTTGATGATCTGTAGTGCT 90
|||||
RESULT 10
US-08-628-686-66
; Sequence 66, Application US/08628686
; GENERAL INFORMATION:
; APPLICANT: Tabler, Martin
; TITLE OF INVENTION: ASYMMETRIC HAMMERHEAD RIBOZOMES AND
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES FOR THEIR CONSTRUCTION
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hardaway Law Firm
; STREET: P.O. Box 10107 Federal Station
; CITY: Greenville
; STATE: SC
; COUNTRY: USA
; ZIP: 29603-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,686
; FILING DATE: 30-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03391
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP EP93/02853
; FILING DATE: 15-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hardaway III, John B.
; REGISTRATION NUMBER: 26,554
; REFERENCE/DOCKET NUMBER: RPE-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 864-233-6700

```



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; TELEFAX: 864-233-2284
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 564 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-628-686-66

Query Match      100.0%; Score 90; DB 10; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
DB 437 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 496
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 497 CTCCTTGGGATGTTGATGATCTGTAGTGCT 526

RESULT 11
PCT-US02-35112-42
; Sequence 42, Application PC/TUS0235112
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 22488-740
; CURRENT APPLICATION NUMBER: PCT/US02/35112
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
PCT-US02-35112-42

Query Match      100.0%; Score 90; DB 1; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
DB 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 12
US-10-003-035-42
; Sequence 42, Application US/10003035
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 22488-712
; CURRENT APPLICATION NUMBER: US/10/003,035
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 75
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-003-035-42

Query Match      100.0%; Score 90; DB 43; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
DB 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 13
US-10-280-915-42
; Sequence 42, Application US/10280915
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: MULTIVALENT VACCINATION USING RECOMBINANT ADENOVIRUS
; FILE REFERENCE: 22488-741
; CURRENT APPLICATION NUMBER: US/10/280,915
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-280-915-42

Query Match      100.0%; Score 90; DB 48; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
DB 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 14
US-10-286-332A-42
; Sequence 42, Application US/10286332A
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: METHOD OF VACCINATION THROUGH SEROTYPE ROTATION
; FILE REFERENCE: 22488-738
; CURRENT APPLICATION NUMBER: US/10/286,332A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 42
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-286-332A-42

Query Match      100.0%; Score 90; DB 48; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCCACCATG 60
Db 1 ATGAGAGTGAAGGAGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCCACCATG 60

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 15
PCT-US02-35112-47
; Sequence 47, Application PC/TUS0235112
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 22488-740
; CURRENT APPLICATION NUMBER: PCT/US02/35112
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 786
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
PCT-US02-35112-47

Query Match      100.0%; Score 90; DB 1; Length 786;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCCACCATG 60
Db 1 ATGAGAGTGAAGGAGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCCACCATG 60

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

Search completed: March 12, 2004, 01:30:49
Job time : 2284.3 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:52:43 ; Search time 562.569 Seconds
(without alignments)
6934.037 Million cell updates/sec

Title: US-10-003-035-74

Perfect score: 90

Sequence: 1 atgagtggaaggagaaata.....tggtgatctgtagtgc 90

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_hg_hum.*

31: em_hg_inv.*

32: em_hg_other.*

33: em_hg_mus.*

34: em_hg_pln.*

35: em_hg_rod.*

36: em_hg_man.*

37: em_hg_vrt.*

38: em_sy.*

39: em_hgto_hum.*

40: em_hgto_mus.*

41: em_hgto_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	105	6	I20806 Sequence 14
2	90	100.0	210	6	I08400 Sequence 1
3	90	100.0	430	14	AF051948 HIV-1 iso
4	90	100.0	430	14	S77333 rev. vpu [h
5	90	100.0	470	14	AF358148 HIV-1 iso
6	90	100.0	1537	14	AF201085 Simian-Hu
7	90	100.0	1537	14	AF201381 Simian-Hu
8	90	100.0	2020	6	AR360238 Sequence
9	90	100.0	2028	6	AR360240 Sequence
10	90	100.0	2060	6	AR360242 Sequence
11	90	100.0	2552	6	I05789 Sequence 8
12	90	100.0	2563	14	AF189159 HIV-1 str
13	90	100.0	2568	14	AY426110 HIV-1 iso
14	90	100.0	2568	14	AY426111 HIV-1 clo
15	90	100.0	2568	14	AY426112 HIV-1 clo
16	90	100.0	2568	14	AY426113 HIV-1 clo
17	90	100.0	2568	14	AY426114 HIV-1 clo
18	90	100.0	2568	14	AY426115 HIV-1 clo
19	90	100.0	2568	14	AY426116 HIV-1 clo
20	90	100.0	2568	14	AY426117 HIV-1 clo
21	90	100.0	2568	14	AY426118 HIV-1 clo
22	90	100.0	2571	6	AR035189 Sequence
23	90	100.0	2571	6	BD182664 ANTI-CD4
24	90	100.0	2571	14	AF358143 HIV-1 clo
25	90	100.0	2571	14	AF358145 HIV-1 clo
26	90	100.0	2598	6	I05783 Sequence 4
27	90	100.0	2691	14	U12030 Human immun
28	90	100.0	2692	14	U12031 Human immun
29	90	100.0	2694	6	I83400 Sequence 1
30	90	100.0	2696	6	AR264703 Sequence
31	90	100.0	2730	6	AR097865 Sequence
32	90	100.0	2945	6	AR365081 Sequence
33	90	100.0	3084	6	I83401 Sequence 2
34	90	100.0	3156	6	E01088 Nucleic aci
35	90	100.0	3156	14	M14100 Human immun
36	90	100.0	3563	6	AR094661 Sequence
37	90	100.0	3563	6	AR382020 Sequence
38	90	100.0	3563	14	K02011 HIV-1 isola
39	90	100.0	3807	6	AR360189 Sequence
40	90	100.0	6031	12	U19867 Cloning vec
41	90	100.0	8560	6	BD268910 Anti-vira
42	90	100.0	8560	6	AX035462 Sequence
43	90	100.0	8932	14	M15654 Human immun
44	90	100.0	8933	6	AR094659 Sequence
45	90	100.0	8933	6	AR382018 Sequence

ALIGNMENTS

RESULT 1	I20806	Sequence 14	105 bp	DNA	linear	PAT 07-OCT-1996
LOCUS	I20806	Sequence 14 from patent US 5516657.				
DEFINITION	I20806					
ACCESSION	I20806					
VERSION	I20806.1	GI:1601161				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1	(bases 1 to 105)				
AUTHORS	Murphy,C.I. and Young,E.					
TITLE	Baculovirus vectors for expression of secretory and membrane-bound proteins					
JOURNAL	Patent: US 5516657-A 14 14-MAY-1996					

Pred. No. is the number of results predicted by chance to have a

AUTHORS Li,Q.-G., Zhang,Y.-J. and Wadell,G.
TITLE Direct Submission
JOURNAL Submitted (02-MAR-1998) Virology, Umea University, Umea S-901 85, Sweden

FEATURES
source
1. .430
/organism="Human immunodeficiency virus 1"
/mol_type="genomic DNA"
/isolate="BC9101"
/db_xref="taxon:11676"
/cell_line="Jurkat-tat III"
/country="China"
93. .341
/gene="vpu"
/pseudo
93. .341
/gene="vpu"
/note="no start codon"
/pseudo
/codon_start=1

gene
CDS

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Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 60
Db 256 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 315

Qy 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 316 CTCCTTGGGATGTTGATGATCTGTAGTGCT 345

RESULT 4
S77533
LOCUS S77533 430 bp RNA linear VRL 06-MAY-2003
DEFINITION rev, vpu [human immunodeficiency virus type 1 HIV-1, BC9101, Chinese isolate, Genomic RNA Mutant, 430 nt].
ACCESSION S77533
VERSION S77533.1 GI:957313
KEYWORDS
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
VIRUSES; Retroviral viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 430)
Li,Q.G., Zhang,Y.J., Liang,Y., Peng,C.Q., Li,Y.Z., Sjoberg,R.,
Jiang,Y., Wang,N.F. and Wadell,G.
The morphogenesis of a Chinese strain of HIV-1 forming inclusion
bodies in Jurkat-tat III cells
J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 9 (2), 103-113
(1995)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE 95268877
PUBMED 7749785
REMARK Genbank staff at the National Library of Medicine created this entry [NCBI gisseq 165679] from the original journal article. This sequence comes from Fig. 9.

FEATURES
source
1. .430
/organism="Human immunodeficiency virus 1"
/mol_type="genomic RNA"
/db_xref="taxon:11676"
93. .341
/gene="vpu"
/note="no start codon"

ORIGIN
Query Match 100.0%; Score 90; DB 14; Length 430;
Best Local Similarity 100.0%; Pred. No. 2e-17;

FEATURES
source
1. .105
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 90; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 60
Db 10 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 69

Qy 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 70 CTCCTTGGGATGTTGATGATCTGTAGTGCT 99

RESULT 2
I08400
LOCUS I08400 210 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent WO 8602930.
ACCESSION I08400
VERSION I08400.1 GI:588888
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 210)
AUTHORS Essex,M.E. and Lee,T.-H.
TITLE ASSAY FOR DETECTING INFECTION BY HUMAN T-CELL LYMPHOTROPIC VIRUS
JOURNAL Patent: WO 8602930-A 1 22-MAY-1986;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 60

Qy 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 3
AF051948
LOCUS AF051948 430 bp DNA linear VRL 17-MAR-1998
DEFINITION HIV-1 isolate BC9101 from China, vpu pseudogene, complete sequence.
ACCESSION AF051948
VERSION AF051948.1 GI:2961622
KEYWORDS
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
VIRUSES; Retroviral viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 430)
Li,Q.G., Zhang,Y.J., Liang,Y., Peng,C.Q., Li,Y.Z., Sjoberg,R.,
Jiang,Y., Wang,N.F. and Wadell,G.
The morphogenesis of a Chinese strain of HIV-1 forming inclusion
bodies in Jurkat-tat III cells
J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 9 (2), 103-113
(1995)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE 95268877
PUBMED 7749785
REFERENCE 2 (bases 1 to 430)

JOURNAL with live-virus vaccine and challenged with pathogenic SHIVKU-1
MEDLINE AIDS Res. Hum. Retroviruses 16 (15), 1573-1580 (2000)
PUBMED 20507321
11054270
REFERENCE 2 (bases 1 to 1537)
AUTHORS Stipp,H.L., Kumar,A. and Narayan,O.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1999) Microbiology, Molecular Genetics and
Immunology, University of Kansas Medical Center, 3901 Rainbow Blvd,
Kansas City, KS 66160, USA

FEATURES
source
1. .1537
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/strain="KU-1/105w98"
/db_xref="taxon:57667"
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/note="gp120"
/codon_start=1
/product="envelope glycoprotein"
/protein_id="AAF13720.1"
/db_xref="GI:6470327"
/translation="MRVKEKYCHLRWGRWGTMGLGMLTCSATEKLVTVVYGVV
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RAKWNDTLQIASLREQFGNNKTIIFKSSGGDPEIVTHSFGCGEFPYCNSTQLEN
STWFNSTWSTERSNTEGSNTILPCRIKQIINWQVKVAMYPPIISGQIRCSNIT
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EKRA"

ORIGIN
Query Match 100.0%; Score 90; DB 14; Length 1537;
Best Local Similarity 100.0%; Pred. No. 1.9e-17; Mismatches 0; Indels 0; Gaps 0;
Matches 90; Conservative 0

Qy 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
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Qy 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 8
AR360238 AR360238 2020 bp DNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 135 from patent US 6596279.
ACCESSION AR360238
VERSION AR360238.1 GI:33767119
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2020)
AUTHORS Paoletti,E., Tartaglia,J., Cox,W.I., Gallo,R. and Franchini,G.
TITLE Immunodeficiency recombinant poxvirus
JOURNAL Patent: US 6596279-A 135 22-JUL-2003;
FEATURES Location/Qualifiers
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JOURNAL with live-virus vaccine and challenged with pathogenic SHIVKU-1
MEDLINE AIDS Res. Hum. Retroviruses 16 (15), 1573-1580 (2000)
PUBMED 20507321
11054270
REFERENCE 2 (bases 1 to 1537)
AUTHORS Stipp,H.L., Kumar,A. and Narayan,O.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1999) Microbiology, Molecular Genetics and
Immunology, University of Kansas Medical Center, 3901 Rainbow Blvd,
Kansas City, KS 66160, USA

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RESULT 8
AR360238 AR360238 2020 bp DNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 135 from patent US 6596279.
ACCESSION AR360238
VERSION AR360238.1 GI:33767119
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2020)
AUTHORS Paoletti,E., Tartaglia,J., Cox,W.I., Gallo,R. and Franchini,G.
TITLE Immunodeficiency recombinant poxvirus
JOURNAL Patent: US 6596279-A 135 22-JUL-2003;
FEATURES Location/Qualifiers
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Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

Qy 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
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Qy 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 357 CTCCTTGGGATGTTGATGATCTGTAGTGCT 386

RESULT 9
AR360240 AR360240 2028 bp DNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 138 from patent US 6596279.
ACCESSION AR360240
VERSION AR360240.1 GI:33767121
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2028)
AUTHORS Paoletti,E., Tartaglia,J., Cox,W.I., Gallo,R. and Franchini,G.
TITLE Immunodeficiency recombinant poxvirus
JOURNAL Patent: US 6596279-A 138 22-JUL-2003;
FEATURES Location/Qualifiers
source
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Best Local Similarity 100.0%; Pred. No. 1.9e-17; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 357 CTCCTTGGGATGTTGATGATCTGTAGTGCT 386

RESULT 10
AR360242 AR360242 2060 bp DNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 141 from patent US 6596279.
ACCESSION AR360242
VERSION AR360242.1 GI:33767123
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2060)
AUTHORS Paoletti,E., Tartaglia,J., Cox,W.I., Gallo,R. and Franchini,G.
TITLE Immunodeficiency recombinant poxvirus
JOURNAL Patent: US 6596279-A 141 22-JUL-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.9e-17; Mismatches 0; Indels 0; Gaps 0;
Matches 90; Conservative 0

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Db 297 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 356
Qy 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

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Db      357 CTCTTGGGATGTGATGATCTGTAGTGCT 386

RESULT 11
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LOCUS      I05789      2552 bp      DNA      linear      PAT 02-DEC-1994
DEFINITION Sequence 8 from Patent EP 0272858.
ACCESSION I05789
VERSION   I05789.1 GI:590911
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 2552)
AUTHORS   Rusche, J., Lynn, D., Carson, H., Putney, S. and Jellis, C.L.
TITLE     Recombinant HIV envelope proteins produced in insect cells
JOURNAL   Patent: EP 0272858-A2 8 29-JUN-1988;
FEATURES   Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 CTCTTGGGATGTGATGATCTGTAGTGCT 90
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Db      61 CTCTTGGGATGTGATGATCTGTAGTGCT 90
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RESULT 12
AF189159
LOCUS      AF189159      2563 bp      DNA      linear      VRL 17-JAN-2000
DEFINITION HIV-1 strain IIBx clone S10 envelope polyprotein variant (env)
            gene, complete cds.
ACCESSION AF189159
VERSION   AF189159.1 GI:6707314
KEYWORDS
SOURCE    Human immunodeficiency virus 1 (HIV-1)
ORGANISM  Human immunodeficiency virus 1
REFERENCE 1 (bases 1 to 2563)
AUTHORS   Hoffman, T.L., LaBrache, C.C., Zhang, W., Canziani, G., Robinson, J.,
            Chaiken, I., Hoxie, J.A. and Doms, R.W.
TITLE     Stable exposure of the coreceptor-binding site in a CD4-independent
            HIV-1 envelope protein
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (11), 6359-6364 (1999)
MEDLINE   99272698
PUBMED    10339592
REFERENCE 2 (bases 1 to 2563)
AUTHORS   LaBrache, C.C., Hoffman, T.L., Romano, J., Haggarty, B.S.,
            Edwards, T.G., Matthews, T.J., Doms, R.W. and Hoxie, J.A.
TITLE     Determinants of CD4 independence for a human immunodeficiency virus
            type 1 variant map outside regions required for coreceptor
            specificity
JOURNAL   J. Virol. 73 (12), 10310-10319 (1999)
MEDLINE   20027260
PUBMED    10559349
REFERENCE 3 (bases 1 to 2563)
AUTHORS   LaBrache, C.C., Hoffman, T.L., Romano, J., Haggarty, B.S.,
            Edwards, T.G., Matthews, T.J., Doms, R.W. and Hoxie, J.A.
TITLE     Direct Submission
JOURNAL   Submitted (23-SEP-1999) Surgery, Duke University, 117 SORF, LaSalle
            Street Extension, Durham, NC 27710, USA
FEATURES   Location/Qualifiers
            source
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Query Match      100.0%; Score 90; DB 14; Length 2563;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
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Qy      61 CTCTTGGGATGTGATGATCTGTAGTGCT 90
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RESULT 13
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LOCUS      AY426110      2568 bp      DNA      linear      VRL 29-OCT-2003
DEFINITION HIV-1 isolate BaL from USA envelope glycoprotein (env) gene,
            complete cds.
ACCESSION AY426110
VERSION   AY426110.1 GI:37962965
KEYWORDS
SOURCE    Human immunodeficiency virus 1 (HIV-1)
ORGANISM  Human immunodeficiency virus 1
REFERENCE 1 (bases 1 to 2568)
AUTHORS   Pastore, C., Ramos, A. and Mosier, D.E.
TITLE     Coreceptor switching by HIV-1 is impeded by loss of fitness
            Unpublished
JOURNAL   2 (bases 1 to 2568)
REFERENCE 2 (bases 1 to 2568)
AUTHORS   Pastore, C., Ramos, A. and Mosier, D.E.
TITLE     Direct Submission
JOURNAL   Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research
            Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
FEATURES   Location/Qualifiers
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QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 14
LOCUS AY426111 2568 bp DNA linear VRL 29-OCT-2003
DEFINITION HIV-1 clone Bal-lp isolate Bal from USA envelope glycoprotein (env)
ACCESSION AY426111
VERSION AY426111.1 GI:37962967
KEYWORDS gene, complete cds.
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
REFERENCE 1 (bases 1 to 2568)
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.
TITLE Coreceptor switching by HIV-1 is impeded by loss of fitness
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2568)
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.
TITLE Direct Submission
JOURNAL Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA

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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 15
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DEFINITION HIV-1 clone Bal-1A isolate Bal from USA envelope glycoprotein (env)
ACCESSION AY426112
VERSION AY426112.1 GI:37962969
KEYWORDS gene, complete cds.
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
REFERENCE 1 (bases 1 to 2568)
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.
TITLE Coreceptor switching by HIV-1 is impeded by loss of fitness
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2568)
AUTHORS Pastore,C., Ramos,A. and Mosier,D.E.
TITLE Direct Submission
JOURNAL Submitted (02-OCT-2003) Dept. of Immunology, The Scripps Research
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGAGAGTGAAGGAGAATATCAGCACCTTGTGGAGATGGGGGTGGAGATGGGCACCATG 60
Db      1  ATGAGAGTGAAGGAGAATATCAGCACCTTGTGGAGATGGGGGTGGAGATGGGCACCATG 60

Qy      61  CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:51:27 ; Search time 212.202 Seconds
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Title: US-10-003-035-74

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Searched: 3373863 seqs, 2124099041 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	90	100.0	210	1	AA092594
6	90	100.0	486	9	ADB87770
7	90	100.0	486	9	Add66292
8	90	100.0	564	2	AAQ87557
9	90	100.0	564	2	AAQ87555
10	90	100.0	615	9	ADB87771
11	90	100.0	615	9	Add66293
12	90	100.0	786	9	ADB87776
13	90	100.0	786	9	Add66298
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19	90	100.0	1308	9	Add66287
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33	90	100.0	3084	2	AAV09365
34	90	100.0	3156	1	AA060128
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36	90	100.0	3157	9	Add66265
37	90	100.0	3417	9	ADB87750
38	90	100.0	3417	9	Add66272
c 39	90	100.0	3808	2	AAT04701
c 40	90	100.0	3808	2	AAV58244
c 41	90	100.0	3808	2	AAV60252
42	90	100.0	3839	9	ADB87781
43	90	100.0	3839	9	Add66303
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45	90	100.0	4040	9	Add66305

ALIGNMENTS

RESULT 1

ADB87801	ID	ADB87801	standard; DNA; 90 BP.
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XX	DT	04-DEC-2003	(first entry)
XX	DE	gp120	signal peptide DNA fragment.
XX	KW	adenovirus; HIV antigen; infection; anti-HIV, virucide; antibacterial;	
XX	KW	antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;	
XX	KW	pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.	
XX	OS	Human immunodeficiency virus 1.	
XX	PN	US2002155127-A1.	
XX	PD	24-OCT-2002.	
XX	PF	01-NOV-2001; 2001US-00003035.	
XX	PR	02-JUN-2000; 2000US-00585599.	
XX	PR	04-JUN-2001; 2001WO-US018238.	
XX	PA	(WANG/) WANG D.	
XX	PI	Wang D;	
XX	DR	WPI; 2003-182621/18.	
XX	PT	New recombinant adenoviruses, useful as vaccines for eliciting immune	
XX	PT	response or conferring protection against infection of a pathogenic	
XX	PT	antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor	
XX	PT	antigens.	
XX	PS	Claim 21; Page 81; 156pp; English.	
XX	CC	This invention describes a novel recombinant adenovirus comprising an HIV	
XX	CC	sequence encoding an HIV antigen, where expression of the HIV antigen by	
XX	CC	the recombinant adenovirus elicits an immune response directed against	
XX	CC	the HIV antigen in a host upon infection of the host by the recombinant	
XX	CC	adenovirus. The products of the invention have anti-HIV, virucide,	
XX	CC	antibacterial, antiparasitic, protozoacide, cytostatic and	
XX	CC	immunomodulatory activity. The recombinant adenoviruses are useful as	
XX	CC	vaccines for eliciting immune response or conferring protection against	

CC infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the invention.

XX

SQ Sequence 90 BP; 22 A; 11 C; 34 G; 23 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.7e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
Db 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60

Qy 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 2

ADD66325
ID ADD66325 standard; DNA; 90 BP.
XX
AC ADD66325;
XX
DT 15-JAN-2004 (first entry)
XX
DE HIV gp120 signal peptide DNA.
XX
KW virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
KW respiratory syncytial virus; herpes simplex virus; human papilloma virus; HIV infection; ds.
XX
OS Human immunodeficiency virus.
XX
FN US2003138459-A1.
XX
PD 24-JUL-2003.
XX
PF 17-MAR-2003; 2003US-00286332.
XX
PR 02-JUN-2000; 2000US-00585599.
PR 04-JUN-2001; 2001WO-US018238.
PR 01-NOV-2001; 2001US-00003035.
XX
PA (WANG/) WANG D.
XX
PI Wang D;
XX
XX WPI; 2003-851718/79.
XX
DR Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprises administering to the host a first and a second recombinant adenovirus.
XX
PS Example; SEQ ID NO 74; 185pp; English.
XX
CC The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.
XX
SQ Sequence 90 BP; 22 A; 11 C; 34 G; 23 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.7e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
Db 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60

Qy 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 3

AAT15319
ID AAT15319 standard; DNA; 105 BP.
XX
AC AAT15319;
XX
DT 25-MAR-2003 (revised)
DT 18-NOV-1996 (first entry)
XX
DE pVLS2p67120 fragment.
XX
KW Baculovirus vector; p67 signal sequence; insect cell; promoter; egt gene; insect virus; Autographa californica nuclear polyhedrosis virus; AcMNPV; Sf9 cell; glycosylated protein production; HIV-1 gp120; envelope protein; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 10..105
FT sig_peptide /tag= a
FT /tag= b
FT /note= "p67 signal peptide"
FT mat_peptide 100..105
FT /tag= c
FT /note= "HIV-1 gp120 fragment"
XX
PN US5516657-A.
XX
PD 14-MAY-1996.
XX
PF 05-MAR-1993; 93US-00029402.
XX
PR 11-MAY-1992; 92US-00880647.
XX
PA (CAMP-) CAMBRIDGE BIOTECH CORP.
XX
PI Young E, Murphy CI;
XX
XX WPI; 1996-251008/25.
XX P-PSDB; AAR95884.
XX
DR Baculovirus vectors comprising a signal peptide and promoter - for improved expression and secretion of glycosylated proteins, e.g., HIV-1 gp120, in the late term of Baculovirus infection.
XX
PS Example 3; Col 21-24; 35pp; English.
XX
CC This sequence represents a fragment of a baculovirus vector of the invention. The vectors are for the expression and secretion of foreign proteins in an insect cell. The vectors comprise a baculovirus promoter operably linked to an insect virus signal peptide coding region from a baculovirus protein. The signal peptide is either the baculovirus glycoprotein p67 signal peptide, or the signal peptide from the 60 kD protein of the Autographa californica nuclear polyhedrosis virus (AcMNPV) egt gene. The baculovirus vectors can be used to generate recombinant virus for protein expression in Sf9 cells in a batch type system. The vectors allow for the production of proteins that are glycosylated and secreted in the late term of infection, when the promoter is most active.

CC The glycosylated proteins are produced at a much higher level than in
 CC previous systems. These vectors can be used to produce HIV-1 gp120, and
 CC other envelope proteins. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 105 BP; 28 A; 14 C; 37 G; 26 T; 0 U; 0 Other;
 Query Match 100.0%; Score 90; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 8e-20;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
 DB 10 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 69
 QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
 DB 70 CTCCTTGGGATGTTGATGATCTGTAGTGCT 99
 RESULT 4
 AAT01088
 ID AAT01088 standard; cDNA; 119 BP.
 XX
 AC AAT01088;
 DT 26-MAR-1996 (first entry)
 XX
 DE V1Jns-gp160IIIB construct junction sequence.
 XX
 KW Polynucleotide vaccine; genetic immunisation; coordinate expression;
 KW HIV-1; AIDS; human immunodeficiency virus; antigen; immunogen;
 KW vector V1Jns; gp160; promoter; terminator; CMVintA-BGH; ds; ss.
 XX
 OS Synthetic.
 XX
 PN WO9524485-A2.
 XX
 PD 14-SEP-1995.
 XX
 PF 03-MAR-1995; 95WO-US002633.
 XX
 PR 07-MAR-1994; 94US-00207526.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Liu MA, Shiver JW, Perry HC;
 XX
 DR WPI; 1995-328276/42.
 XX
 PT New poly-cistronic expression construct - for producing antigens and
 PT immuno-stimulatory gene products useful as vaccines against e.g. HIV,
 PT hepatitis, etc.
 XX
 PS Claim 23; Page 138; 178pp; English.
 XX
 CC The HIV-1 strain IIB gp160 gene was inserted into V1Jns, a vector contg.
 CC a CMVintA-BGH terminator construct (AAT01112) that allows controlled
 CC expression of heterologous genes. The sequences across the 5' junction of
 CC CMVintA (cytomegalovirus promoter and intron A) and the HIV gene, and
 CC across the 3' junction of the HIV gene and BGH (bovine growth hormone)
 CC terminator are given in AAT01088-89. The vector allows large-scale prodn.
 CC of polynucleotide vaccine in bacterial host cells
 XX
 SQ Sequence 119 BP; 33 A; 16 C; 40 G; 30 T; 0 U; 0 Other;
 Query Match 100.0%; Score 90; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 8.2e-20;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
 DB 13 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 72

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
 DB 73 CTCCTTGGGATGTTGATGATCTGTAGTGCT 102
 RESULT 5
 AAN92594
 ID AAN92594 standard; DNA; 210 BP.
 XX
 AC AAN92594;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-JUN-1990 (first entry)
 XX
 DE Nucleotide sequence for the amino terminal portion of the HTLV-III
 DE envelope region gp 160 and gp 120.
 XX
 KW Glycoproteins gp 120 and gp 160; HTLV-III; HTLV-III antibodies;
 KW immunoassay.
 XX
 OS Human lymphotropic virus type III.
 XX
 FH Key Location/Qualifiers
 CDS 1..210
 FT /tag= a
 FT /note= "comprises leader peptide and mature peptide"
 FT misc_feature 1
 FT /tag= c
 FT /note= "corresponds to nucleotide sequence 5802 of the
 HTLV-III genome"
 FT mat_peptide 91..210
 FT /tag= b
 XX
 PN CA1247082-A.
 XX
 PD 20-DEC-1988.
 XX
 PF 12-NOV-1985; 85CA-00495112.
 XX
 PR 09-NOV-1984; 84US-00670361.
 PR 07-NOV-1985; 85US-00795974.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Essex ME;
 XX
 DR WPI; 1989-061499/09.
 DR P-PSDB; AAN94662.
 XX
 PT Human T-cell lymphotropic virus type III - useful for detection of human
 PT T-cell lymphotropic virus type III antibodies.
 XX
 PS Disclosure; Page ?; 27pp; English.
 XX
 CC The polypeptides it encodes are useful for detection of HTLV-III
 CC antibodies by immunoassay methods. Abs. to these polypeptides are useful
 CC as immunoassay reagents for detecting polypeptides in biological
 CC specimens, esp. human lymphocytes or human saliva. (Updated on 25-MAR-
 CC 2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 210 BP; 59 A; 32 C; 64 G; 55 T; 0 U; 0 Other;
 Query Match 100.0%; Score 90; DB 1; Length 210;
 Best Local Similarity 100.0%; Pred. No. 9.5e-20;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
 DB 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
 QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

```

Db      61 CTCCTGGGATGTGATGATCTGTAGTGCT 90

RESULT 6
ADB87770
ID      ADB87770 standard; DNA; 486 BP.
XX
XX
AC      ADB87770;
XX
XX      04-DEC-2003 (first entry)
XX
XX      HIV-1 p17 secreted form DNA SEQ ID 41.
XX
XX      adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
XX      antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;
XX      pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
XX
XX      Human immunodeficiency virus 1.
XX
XX      US2002155127-A1.
XX
XX      24-OCT-2002.
XX
XX      01-NOV-2001; 2001US-00003035.
XX
XX      02-JUN-2000; 2000US-00585599.
XX
XX      04-JUN-2001; 2001WO-US018238.
XX
XX      (WANG/) WANG D.
XX
XX      Wang D;
XX
XX      WPI; 2003-182621/18.
XX
XX      New recombinant adenoviruses, useful as vaccines for eliciting immune
XX      response or conferring protection against infection of a pathogenic
XX      antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
XX      antigens.
XX
XX      Claim 30; Fig 51A; 156pp; English.
XX
XX      This invention describes a novel recombinant adenovirus comprising an HIV
XX      sequence encoding an HIV antigen, where expression of the HIV antigen by
XX      the recombinant adenovirus elicits an immune response directed against
XX      the HIV antigen in a host upon infection of the host by the recombinant
XX      adenovirus. The products of the invention have anti-HIV, virucide,
XX      antibacterial, antiparasitic, protozoacide, cytostatic and
XX      immunomodulatory activity. The recombinant adenoviruses are useful as
XX      vaccines for eliciting immune response or conferring protection against
XX      infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B,
XX      C, D or E or tumor antigens. The recombinant adenoviruses are also
XX      useful as genetic vaccines against pathogenic bacteria, parasites or
XX      protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing
XX      the immunogenicity of the HIV antigens. This sequence represents an HIV-1
XX      strain BH10 antigen construct described in the disclosure of the
XX      invention.
XX
XX      Sequence 486 BP; 183 A; 79 C; 131 G; 93 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 90; DB 9; Length 486;
XX      Best Local Similarity 100.0%; Pred. No. 1.2e-19;
XX      Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGGCCACCATG 60
Db      1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGGCCACCATG 60
XX
QY      61 CTCCTTGGGATGTGATGATCTGTAGTGCT 90
Db      61 CTCCTTGGGATGTGATGATCTGTAGTGCT 90
XX
RESULT 7
QAQ87557
ID      QAQ87557 standard; DNA; 564 BP.
XX
XX      QAQ87557;
XX
XX      04-JAN-1996 (first entry)
XX
XX      Human T cell lymphotropic virus type III bases 5819-6382.
XX

```

KW Human immunodeficiency virus; asymmetric; hammerhead; ribozyme; helix I;
 KW helix II; helix III; loop 2; cleavage site; amplification; PCR; primer;
 KW motif; construct; pathogen; retrovirus infection; ss.
 XX

OS Synthetic.

XX Key Location/Qualifiers
 XX primer_bind 37..53
 FT /*tag= a
 FT /note= "binds primer AR6B"
 FT complement(213..231)
 FT /*tag= b
 FT /note= "binds primer XHOW"

XX WO9510608-A1.

XX 20-APR-1995.

XX 15-OCT-1993; 93WO-EP002853.

XX 15-OCT-1993; 93WO-EP002853.

XX (FORT-) FORT FOUND RES & TECHNOLOGY HELLAS.

XX (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM STIFTUN.

XX Tabler M, Sczakiel G, Homann M;

XX WPI; 1995-161795/21.

XX Asymmetric hammerhead ribozyme(s) and constructs - having high catalytic
 PT activity and improved specificity, for inactivating target RNA e.g. in
 PT unwanted endogenous genes or pathogens.

XX Example 2; Fig 7; 72pp; English.

XX A portion of the human T cell lymphotropic virus type III sequence
 CC (HTLVIII) between bases 5819-6382. The region between bases 37-231 of
 CC this sequence (bases 5855-6050 of the HTLVIII sequence) was amplified
 CC using the primers AAQ87558-9. This amplified region (AAQ87561) was
 CC digested with EcoRI and XhoI and ligated with the plasmid pBS-UCU
 CC (AAQ87563), also digested with EcoRI and XhoI, to generate the asymmetric
 CC ribozyme construct p(alpha)-Rz195 (AAQ87565). The plasmid pBS-UCU is
 CC generated by modification of the Helix I box site of plasmid pBS-Rz120 by
 CC the oligonucleotide UCU (AAQ87562). This is an example of an asymmetric
 CC ribozyme construct generated to recognise and cleave after the sequence
 CC GUC in the target RNA. The construct encodes the asymmetric ribozyme
 CC alpha-Y-Rz195 (AAQ87567) which cleaves the HTLVIII RNA sequence AAQ87566.
 CC The asymmetric ribozymes generated by transcription of the constructs can
 CC be used in treatments to suppress endogenous genes or genes of pathogens
 CC or pathogenic RNA e.g. in viral or retroviral infections such as HIV
 CC infection

XX Sequence 564 BP; 198 A; 93 C; 141 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 2; Length 564;
 Best Local Similarity 100.0%; Pred. No. 1.2e-19;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
 Db 437 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 496

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

Db 497 CTCCTTGGGATGTTGATGATCTGTAGTGCT 526

RESULT 9

AAQ89755

ID AAQ89755 standard; DNA; 564 BP.

XX AAQ89755;

XX

DT 08-FEB-1996 (first entry)
 XX Plasmid pAR6 partial seq. contg. HTLV-III bases 5819-6382.

XX Hammerhead ribozyme; catalytic site; helix; asymmetric; specificity; HIV;
 KW prokaryote; eukaryote; fruit ripening gene; protective agent; fungus;
 KW virus; insect pathogen; transgenic plant; transformed organism; ss.

OS Synthetic.

XX Key Location/Qualifiers
 XX primer_bind 37..53
 FT /*tag= a
 FT /note= "binds primer ARA6B (AAQ89756)"
 FT 213..231
 FT /*tag= b
 FT /note= "binds primers XHOW (AAQ89757) and XHOM
 (AAQ89758)"

XX WO9510609-A1.

XX 20-APR-1995.

XX 14-OCT-1994; 94WO-EP003391.

XX 15-OCT-1993; 93WO-EP002853.

XX (FORT-) FORT FOUND RES & TECHNOLOGY HELLAS.

XX (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM STIFTUN.

XX Tabler M, Sczakiel G, Homann M;

XX WPI; 1995-161796/21.

XX Asymmetric hammerhead ribozymes - and corresp. coding constructs, useful
 PT for inactivation or suppression of target genes, e.g. in pathogens or
 PT during fruit ripening.

XX Example 2; Fig 7A; 83pp; English.

XX The partial sequence of the plasmid pAR6 contg. the human T-cell
 CC lymphotropic virus type III (HTLV-III) bases 5819-6382. The sequence was
 CC used to generate an asymmetric ribozyme able to cleave the GTC (GUC in
 CC RNA) motif at pos. 230-33. The region between bases 37-231 of this
 CC sequence was amplified by the primers AAQ89756-8 and replaced the helix I
 CC sequence of construct pBS29-Rz12 (AAQ89745). The construct generated
 CC (p(alpha)-Rz195; AAQ89761) encodes the ribozyme (alpha)-Y-Rz195
 CC (AAQ89754), which targets and cleaves after the GUC sequence at pos. 6049
 CC -51 of the HTLV-III RNA sequence (AAQ89762). The construct was used in
 CC the generation of an asymmetric ribozyme contg. the catalytic site of a
 CC hammerhead ribozyme and a shortened helix I sequence. The ribozymes
 CC constructed are asymmetric in that they contain serially deleted Helix I
 CC sequences (see AAQ89772-80 for other examples). By interchanging the
 CC helix I and III sequences, the specificity of the ribozymes can be
 CC altered e.g. they can be used to inactivate or suppress target RNAs in
 CC prokaryote or eukaryote cells such as suppressing certain fruit ripening
 CC genes or as protective agents against fungal, viral or insect pathogens
 CC in transgenic plants or transformed organisms

XX Sequence 564 BP; 198 A; 93 C; 141 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 2; Length 564;
 Best Local Similarity 100.0%; Pred. No. 1.2e-19;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
 Db 437 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 496

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

Db 497 CTCCTTGGGATGTTGATGATCTGTAGTGCT 526

RESULT 10
ADB87771
ID ADB87771 standard; DNA; 615 BP.
XX AC ADB87771;
XX DT 04-DEC-2003 (first entry)
XX AC
XX DE HIV-1 p17 membrane form DNA SEQ ID 42.
XX KW adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
XX KW antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;
XX KW pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
XX OS Human immunodeficiency virus 1.
XX PN US200215127-A1.
XX PD 24-OCT-2002.
XX PF 01-NOV-2001; 2001US-00003035.
XX PR 02-JUN-2000; 2000US-00585599.
XX PR 04-JUN-2001; 2001WO-US018238.
XX PA (WANG/) WANG D.
XX PI Wang D;
XX DR WPI; 2003-182621/18.
XX PT New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor antigens.
XX PS Claim 30; Fig 51A; 156pp; English.
XX CC This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the invention.
XX SQ Sequence 615 BP; 217 A; 101 C; 162 G; 135 T; 0 U; 0 Other;
Query Match 100.0%; Score 90; DB 9; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAGTGAAGGAGAAATATCAGCATTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
Db 1 ATGAGAGTGAAGGAGAAATATCAGCATTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
RESULT 11
ADD66293
ID ADD66293 standard; DNA; 615 BP.

XX AC ADD66293;
XX DT 15-JAN-2004 (first entry)
XX DE HIV p17 membrane form DNA.
XX KW virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;
XX KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
XX KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;
XX KW HIV infection; ds; gene.
XX OS Human immunodeficiency virus.
XX PN US2003138459-A1.
XX PD 24-JUL-2003.
XX PF 17-MAR-2003; 2003US-00286332.
XX PR 02-JUN-2000; 2000US-00585599.
XX PR 04-JUN-2001; 2001WO-US018238.
XX PR 01-NOV-2001; 2001US-00003035.
XX PA (WANG/) WANG D.
XX PI Wang D;
XX DR WPI; 2003-851718/79.
XX DR P-PSDB; ADD66296.
XX PT Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprises administering to the host a first and a second recombinant adenovirus.
XX PS Example; SEQ ID NO 42; 185pp; English.
XX CC The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.
XX SQ Sequence 615 BP; 217 A; 101 C; 162 G; 135 T; 0 U; 0 Other;
Query Match 100.0%; Score 90; DB 9; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAGTGAAGGAGAAATATCAGCATTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
Db 1 ATGAGAGTGAAGGAGAAATATCAGCATTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
RESULT 12
ADB87776
ID ADB87776 standard; DNA; 786 BP.
XX AC ADB87776;
XX DT 04-DEC-2003 (first entry)
XX DE HIV-1 p24 secreted form DNA SEQ ID 47.
XX KW adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
KW antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;

PA (WANG/) WANG D.
XX
XX Wang D;
XX WPI; 2003-182621/18.
XX
XX New recombinant adenoviruses, useful as vaccines for eliciting immune
PT response or conferring protection against infection of a pathogenic
PT antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
PT antigens.
XX
XX Claim 30; Page 63; 156pp; English.
XX
XX This invention describes a novel recombinant adenovirus comprising an HIV
CC sequence encoding an HIV antigen, where expression of the HIV antigen by
CC the recombinant adenovirus elicits an immune response directed against
CC the HIV antigen in a host upon infection of the host by the recombinant
CC adenovirus. The products of the invention have anti-HIV, virucide,
CC antibacterial, antiparasitic, protozoacide, cytostatic and
CC immunomodulatory activity. The recombinant adenoviruses are useful as
CC vaccines for eliciting immune response or conferring protection against
CC infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B,
CC C, D or E or tumor antigens. The recombinant adenoviruses are also
CC useful as genetic vaccines against pathogenic bacteria, parasites or
CC protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing
CC the immunogenicity of the HIV antigens. This sequence represents an HIV-1
CC strain BH10 antigen construct described in the disclosure of the
XX invention.
XX
XX Sequence 915 BP; 314 A; 168 C; 229 G; 204 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 90; DB 9; Length 915;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
Db 1 ATGAGAGTGAAGGAGAAATATCAGCACTGTGGAGATGGGGTGGAGATGGGGCACCATG 60

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 15
ADD66299
ID ADD66299 standard, DNA; 915 BP.
XX
XX AC ADD66299;
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE HIV p24 membrane form DNA.
XX
XX KW virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;
KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;
KW HIV infection; ds; gene.
XX
XX OS Human immunodeficiency virus.
XX
XX PN US2003138459-A1.
XX
XX PD 24-JUL-2003.
XX
XX PF 17-MAR-2003; 2003US-00286332.
XX
XX PR 02-JUN-2000; 2000US-00585599.
PR 04-JUN-2001; 2001WO-US018238.
PR 01-NOV-2001; 2001US-00003035.
XX
XX (WANG/) WANG D.
XX

PI Wang D;
XX
XX WPI; 2003-851718/79.
DR P-PSDB; ADD66302.
XX
XX Enhancing the immunity of a host to infection of a first and second
PT pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or
PT HIV infections comprises administering to the host a first and a second
PT recombinant adenovirus.
XX
XX Example; SEQ ID NO 48; 185pp; English.
XX
XX The invention relates to a method of enhancing the immunity of a host to
CC infection of a first and second pathogenic virus comprising administering
CC to the host a first and a second recombinant adenovirus. The method is
CC useful for enhancing immunity of the host to infections, e.g. influenza,
CC Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes
CC simplex or human papilloma virus or HIV infections. The present sequence
CC is used in the exemplification of the invention.
XX
XX Sequence 915 BP; 314 A; 168 C; 229 G; 204 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 90; DB 9; Length 915;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTGTGGAGATGGGGTGGAGATGGGGCACCATG 60
Db 1 ATGAGAGTGAAGGAGAAATATCAGCACTGTGGAGATGGGGTGGAGATGGGGCACCATG 60

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

Search completed: March 11, 2004, 20:49:40
Job time : 214.202 Secs

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:51:27 ; Search time 254.642 Seconds
(without alignments)
1801.765 Million cell updates/sec

Title: US-10-003-035-25

Perfect score: 108
Sequence: 1 tctacaagaccacacacaa.....atatgagacaagcacattgt 108

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002s:*

7: geneseqn2003as:*

8: geneseqn2003bs:*

9: geneseqn2003cs:*

10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	108	100.0	108	9	ADB87754 HIV-1 BH1
2	108	100.0	108	9	Add66276 Multi-cla
3	108	100.0	288	1	AAN90622 Sequence
4	108	100.0	288	2	AAQ04273 Sub 1, a
5	108	100.0	423	1	AAN90623 Sequence
6	108	100.0	423	2	AAQ04274 Sub 2, a
7	108	100.0	536	1	AAN92108 Synthetic
8	108	100.0	536	1	AAN90626 N-termina
9	108	100.0	537	1	AAN90739 DNA encod
10	108	100.0	537	1	AAN92116 Polynucle
11	108	100.0	702	1	AAN92112 Polynucle
12	108	100.0	702	1	AAN92112 Polynucle
13	108	100.0	702	2	AAQ35897 Recombina
14	108	100.0	1056	1	AAN92109 Synthetic
15	108	100.0	1059	1	AAN90740 DNA encod
16	108	100.0	1059	1	AAN92117 Polynucle
17	108	100.0	1269	1	AAN90738 DNA encod
18	108	100.0	1269	1	AAN92115 Polynucle
19	108	100.0	1276	1	AAN92107 Synthetic
20	108	100.0	1533	7	ACC70121 Nucleotid
21	108	100.0	1791	1	AAN90741 DNA encod
22	108	100.0	1791	1	AAN92118 Sequence
23	108	100.0	1796	1	AAN92110 Synthetic

24	108	100.0	1920	1	AAN81452 Sequence
25	108	100.0	2280	9	ADB87745 HIV-1 str
26	108	100.0	2280	9	Add66267 HIV clone
27	108	100.0	2457	1	AAN81451 Sequence
28	108	100.0	2562	9	ADB87761 HIV-1 BH1
29	108	100.0	2562	9	Add66283 Modified
30	108	100.0	2583	9	ADB87753 HIV-1 BH1
31	108	100.0	2583	9	Add66275 HIV E_m/E
32	108	100.0	2673	1	AAN81449 Sequence
33	108	100.0	2747	9	ADB87752 HIV-1 BH1
34	108	100.0	2747	9	Add66274 HIV E_m/E
35	108	100.0	2945	2	AAT05127 HIV virus
36	108	100.0	2950	9	ADB87751 HIV-1 BH1
37	108	100.0	2950	9	Add66273 HIV E_m/E
38	108	100.0	3157	9	ADB87743 HIV-1 str
39	108	100.0	3157	9	Add66265 HIV clone
40	108	100.0	3417	9	ADB87750 HIV-1 BH1
41	108	100.0	3417	9	Add66272 HIV Env m
42	108	100.0	3839	9	ADB87781 HIV-1 mod
43	108	100.0	3839	9	Add66303 Modified
44	108	100.0	4040	9	ADB87783 HIV-1 mod
45	108	100.0	4040	9	Add66305 Modified

ALIGNMENTS

RESULT 1
ADB87754
ID ADB87754 standard; DNA; 108 BP.
XX
AC ADB87754;
XX
DT 04-DEC-2003 (first entry)
XX
DE HIV-1 BH10 V3 loop clade B SEQ ID 25.
XX
KW adenovirus; HIV antigen; infection; anti-HIV, virucide; antibacterial;
KW antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;
KW pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
XX
OS Human immunodeficiency virus 1.
XX
PN US2002155127-A1.
XX
PD 24-OCT-2002.
XX
PF 01-NOV-2001; 2001US-00003035.
XX
PR 02-JUN-2000; 2000US-00585599.
XX
PA 04-JUN-2001; 2001WO-US018238.
XX
(WANG/) WANG D.
XX
Wang D;
XX
WPI; 2003-182621/18.
XX
New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor antigens.

Claim 17; Fig 48; 156pp; English.

This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against

CC infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B,
CC C, D or E or tumour antigens. The recombinant adenoviruses are also
CC useful as genetic vaccines against pathogenic bacteria, parasites or
CC protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing
CC the immunogenicity of the HIV antigens. This sequence represents an HIV-1
CC strain BH10 antigen construct described in the disclosure of the
CC invention.

XX SQ Sequence 108 BP; 48 A; 18 C; 23 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 108; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGGACCGAGGAGA 60
DB 1 TGTACAAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGGACCGAGGAGA 60
QY 61 GCATTGTTTACAATAGGAAAAATAGGAAAAATATGAGACAAGCATTGT 108
DB 61 GCATTGTTTACAATAGGAAAAATAGGAAAAATATGAGACAAGCATTGT 108

RESULT 2

ADD66276
ID ADD66276 standard; DNA; 108 BP.

AC ADD66276;

XX 15-JAN-2004 (first entry)

XX Multi-clade HIV V3 loop clade B.

XX virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;
KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;
KW HIV infection; ds.

XX Human immunodeficiency virus.

XX US2003138459-A1.

XX 24-JUL-2003.

XX 17-MAR-2003; 2003US-00286332.

XX 02-JUN-2000; 2000US-00585599.

PR 04-JUN-2001; 2001WO-US018238.

PR 01-NOV-2001; 2001US-00003035.

XX (WANG/) WANG D.

XX Wang D;

XX WPI; 2003-851718/79.

XX Enhancing the immunity of a host to infection of a first and second
XX pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or
XX HIV infections comprises administering to the host a first and a second
XX recombinant adenovirus.

XX Example; SEQ ID NO 25; 185pp; English.

XX The invention relates to a method of enhancing the immunity of a host to
XX infection of a first and second pathogenic virus comprising administering
XX to the host a first and a second recombinant adenovirus. The method is
XX useful for enhancing immunity of the host to infections, e.g. influenza,
XX Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes
XX simplex or human papilloma virus or HIV infections. The present sequence
XX is used in the exemplification of the invention.

XX Sequence 108 BP; 48 A; 18 C; 23 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 108; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGGACCGAGGAGA 60
DB 1 TGTACAAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGGACCGAGGAGA 60

QY 61 GCATTGTTTACAATAGGAAAAATAGGAAAAATATGAGACAAGCATTGT 108
DB 61 GCATTGTTTACAATAGGAAAAATAGGAAAAATATGAGACAAGCATTGT 108

RESULT 3

AAN90622
ID AAN90622 standard; DNA; 288 BP.

XX AAN90622;

XX 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 22-JUN-1990 (first entry)

XX Sequence encoding Sub1 HIV fusion protein.

XX HIV; AIDS; Sub 1 fusion protein; HIV vaccine; ds.

XX Simian-Human immunodeficiency virus.

XX Key Location/Qualifiers

FT Misc_feature 91..254

FT /*tag= a

FT /label= HIV derived sequence

XX EP305219-A.

XX 08-MAR-1989.

XX 25-AUG-1988; 88EP-00307889.

XX 27-AUG-1987; 87US-00090080.

XX (REPK) REPLIGEN CORP.

XX Rusche JR, Putney SD, Jayaheerian K, Farley J, Grimaila R, Lynn D;

XX Petro J, Okeiffe T;

XX WPI; 1989-070387/10.

XX P-PSDB; AAP94760.

XX New HIV proteins and peptide(s) - used in diagnosis, prophylaxis or

XX therapy of AIDS, esp. for prepn. of vaccines against HIV infection.

XX Claim 1; Table 2; 29pp; English.

XX Protein derivative stimulates a lymphocyte proliferative response in HIV-
XX infected humans, providing a means of diagnosis, protection and
XX therapeutic value. (Updated on 25-MAR-2003 to correct PR field.) (Updated
XX on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
XX standardise OS field)

XX Sequence 288 BP; 106 A; 57 C; 67 G; 58 T; 0 U; 0 Other;

Query Match 100.0%; Score 108; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.2e-22;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGGACCGAGGAGA 60
DB 115 TGTACAAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGGACCGAGGAGA 174

QY 61 GCATTGTTTACAATAGGAAAAATAGGAAAAATATGAGACAAGCATTGT 108
|||||

```

Db      175 GCATTGTTACATAGCAAAATAGGAATATGAGACAGCACATTGT 222

RESULT 4
AAQ04273
ID      AAQ04273 standard; DNA; 288 BP.
XX
XX      AC      AAQ04273;
XX
XX      DT      25-MAR-2003 (revised)
XX      DT      20-SEP-1990 (first entry)
XX
XX      DE      Sub 1, a HIV fusion protein encoding sequence.
XX
XX      KW      HIV; fusion protein; Sub 1; therapy; AIDS; principal neutralising domain;
XX      KW      antibodies; diagnosis; prophylaxis; ss.
XX
XX      OS      Synthetic.
XX
XX      FH      Key      Location/Qualifiers
XX      CDS      1..288
XX      FT      /*tag= a
XX      FT      /product= "HIV 10 kD fusion protein"
XX      FT      /note= "Sub 1"
XX      FT      Region    91..253
XX      FT      /*tag= b
XX      FT      /*label= HIV portion of Sub 1
XX
XX      PN      WO9003984-A.
XX
XX      PD      19-APR-1990.
XX
XX      PF      03-OCT-1988; 88US-00252949.
XX
XX      PR      03-OCT-1988; 88US-00252949.
XX      PR      01-JUN-1989; 89US-00359543.
XX      PR      19-SEP-1989; 89US-00407663.
XX
XX      PA      (REPK ) REPLIGEN CORP.
XX
XX      PI      Rusche JR, Putney SD, Javaherian K, Farley J, Grimaila R;
XX      PI      Lynn DU, Petrobre J;
XX
XX      DR      WPI; 1990-147824/19.
XX      DR      P-PSDB; AAR04492.
XX
XX      PT      Principal neutralising domain of HIV variants - used for producing
XX      PT      peptide(s) and antibodies for diagnosis, prophylaxis and/or therapy
XX      PT      therapy therapy of HIV infection.
XX
XX      PS      Disclosure; Page ?; 108pp; English.
XX
XX      CC      The gene can be expressed in simian cells, and synthesis of HIV proteins
XX      CC      can be detected immunologically. The recombinant protein product
XX      CC      comprises a principal neutralising domain. The neutralising domain is
XX      CC      bounded by cysteine residues which occur at positions 286 and 331, the
XX      CC      segments between the residues form a loop. See also AAR04427-R04506 and
XX      CC      AAQ04273-Q04279. (Updated on 25-MAR-2003 to correct PR field.) (Updated
XX      CC      on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct
XX      CC      PI field.)
XX
XX      SQ      Sequence 288 BP; 106 A; 57 C; 67 G; 58 T; 0 U; 0 Other;

Query Match      100.0%; Score 108; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.2e-22;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TGTACAGACCCCAACAATACAGAAAGTATCCGTATCCAGAGAGGACGAGGAGA 60
Db      115 TGTACAGACCCCAACAATACAGAAAGTATCCGTATCCAGAGAGGACGAGGAGA 174
Qy      61 GCATTGTTACATAGCAAAATAGGAATATGAGACAGCACATTGT 108

Query Match      100.0%; Score 108; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.2e-22;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TGTACAGACCCCAACAATACAGAAAGTATCCGTATCCAGAGAGGACGAGGAGA 60
Db      115 TGTACAGACCCCAACAATACAGAAAGTATCCGTATCCAGAGAGGACGAGGAGA 174
Qy      61 GCATTGTTACATAGCAAAATAGGAATATGAGACAGCACATTGT 108

RESULT 5
AAQ04273
ID      AAQ04273 standard; DNA; 423 BP.
XX
XX      AC      AAQ04273;
XX
XX      DT      24-OCT-2003 (revised)
XX      DT      25-MAR-2003 (revised)
XX      DT      22-JUN-1990 (first entry)
XX
XX      DE      Sequence encoding Sub2 HIV fusion protein.
XX
XX      KW      HIV; AIDS; Sub2 fusion protein; HIV vaccine; ds.
XX
XX      OS      Simian-Human immunodeficiency virus.
XX
XX      FH      Key      Location/Qualifiers
XX      CDS      91..408
XX      FT      /*tag= a
XX      FT      /label= HIV derived sequence
XX
XX      PN      EP306219-A.
XX
XX      PD      08-MAR-1989.
XX
XX      PF      25-AUG-1988; 88EP-00307889.
XX      PR      27-AUG-1987; 87US-00090080.
XX
XX      PA      (REPK ) REPLIGEN CORP.
XX
XX      PI      Rusche JR, Putney SD, Javaherian K, Farley J, Grimaila R, Lynn D;
XX      PI      Petro J, Okeeffe T;
XX
XX      DR      WPI; 1989-070387/10.
XX      DR      P-PSDB; AAP94801.
XX
XX      PT      New HIV proteins and peptide(s) - used in diagnosis, prophylaxis or
XX      PT      therapy of AIDS, esp. for prepn. of vaccines against HIV infection.
XX
XX      PS      Claim 1; Table 3; 29pp; English.
XX
XX      CC      Protein derivative stimulates a lymphocyte proliferative response in HIV-
XX      CC      infected humans, providing a means of diagnosis, protection and
XX      CC      therapeutic value. (Updated on 25-MAR-2003 to correct PR field.) (Updated
XX      CC      on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
XX      CC      standardise OS field)
XX
XX      SQ      Sequence 423 BP; 162 A; 74 C; 89 G; 98 T; 0 U; 0 Other;

Query Match      100.0%; Score 108; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 9.7e-22;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TGTACAGACCCCAACAATACAGAAAGTATCCGTATCCAGAGAGGACGAGGAGA 60
Db      115 TGTACAGACCCCAACAATACAGAAAGTATCCGTATCCAGAGAGGACGAGGAGA 174
Qy      61 GCATTGTTACATAGCAAAATAGGAATATGAGACAGCACATTGT 108

Query Match      100.0%; Score 108; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 9.7e-22;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TGTACAGACCCCAACAATACAGAAAGTATCCGTATCCAGAGAGGACGAGGAGA 60
Db      115 TGTACAGACCCCAACAATACAGAAAGTATCCGTATCCAGAGAGGACGAGGAGA 174
Qy      61 GCATTGTTACATAGCAAAATAGGAATATGAGACAGCACATTGT 108

RESULT 6
AAQ04274
ID      AAQ04274 standard; DNA; 423 BP.
XX
XX      AC      AAQ04274;
XX
XX      DT      25-MAR-2003 (revised)

```

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DT 20-SEP-1990 (first entry)
XX Sub 2, a HIV fusion protein encoding sequence.
DE HIV; fusion protein; Sub 2; therapy; AIDS; principal neutralising domain;
XX antibodies; diagnosis; prophylaxis; ss.
KW Synthetic.
OS
XX
FH Key Location/Qualifiers
FT CDS 1..423
FT FT /*tag= a
FT FT /product= "HIV 18 kD fusion protein"
FT FT /note= "Sub 2"
FT FT 91..407
FT FT /*tag= b
FT FT /label= HIV portion of Sub 2
XX
XX WO9003984-A.
XX
XX 19-APR-1990.
XX
XX 03-OCT-1988; 89US-00252949.
XX
XX 03-OCT-1988; 88US-00252949.
XX
XX 01-JUN-1989; 89US-00359543.
XX
XX 19-SEP-1989; 89US-00407663.
XX
XX (REPK ) REPLIGEN CORP.
XX
XX Rusche JR, Putney SD, Javaherian K, Farley J, Grimalia R;
XX Lynn DU, Petrebre J;
XX WPI; 1990-147824/19.
XX P-FSDB; AAR04493.
XX
XX Principal neutralising domain of HIV variants - used for producing
XX peptide(s) and antibodies for diagnosis, prophylaxis and/or therapy
XX therapy of HIV infection.
XX
XX Disclosure; Page ?; 108pp; English.
XX
XX The gene can be expressed in simian cells, and synthesis of HIV proteins
XX can be detected immunologically. The recombinant protein product
XX comprises a principal neutralising domain. The neutralising domain is
XX bounded by cysteine residues which occur at positions 296 and 331. The
XX segments between the residues form a loop. See also AAR04427-R04506 and
XX AAQ04273-Q04279. (Updated on 25-MAR-2003 to correct PR field.) (Updated
XX on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 423 BP; 162 A; 74 C; 89 G; 98 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 108; DB 2; Length 423;
XX Best Local Similarity 100.0%; Pred. No. 9.7e-22;
XX Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TGTACAGACCCCAACAATACAGAAAAGTATCCGTATCCAGAGGACCGAGGAGA 60
XX 115 TGTACAGACCCCAACAATACAGAAAAGTATCCGTATCCAGAGGACCGAGGAGA 174
XX
XX 61 GCATTGTGTACATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
XX 175 GCATTGTGTACATAGGAAAATAGGAAATATGAGACAAGCACATTGT 222
XX
XX RESULT 7
XX AAN92108
XX ID AAN92108 standard; DNA; 536 BP.
XX
XX AC AAN92108;
XX
XX 25-MAR-2003 (revised)
XX
DT 20-SEP-1990 (revised)
XX 02-MAR-1990 (first entry)
XX
XX Synthetic polynucleotide encoding HTLV-III gpl20 envelope protein.
XX
XX HTLV-III envelope protein gpl20; pPB1; PBI;
XX lymphocyte proliferative response; AIDS.
XX
XX Synthetic.
XX
XX OS
XX
XX AU8821172-A.
XX
XX 13-APR-1989.
XX
XX 18-AUG-1988; 88AU-00021172.
XX
XX 09-OCT-1987; 87US-00107231.
XX
XX (REPK ) REPLIGEN CORP.
XX
XX Putney SD, Lynn D, Javaherian K, Mueller WT, Farley J;
XX WPI; 1989-157957/22.
XX
XX Recombinant human T-cell leukaemia virus 3 proteins - used for
XX stimulating lymphocyte proliferative response and in diagnosis
XX prophylaxis or therapy of AIDS.
XX
XX Example 4; Table 5; 85pp; English.
XX
XX It is a synthetic fragment which encodes a portion of HTLV-III gpl20
XX envelope protein. It has a blunt end on the 5' end and a CTAG overhang on
XX the non-coding strand at the 3' end which will ligate with BamHI. Used in
XX example to construct pPB1 which is used to express the recombinant HTLV-
XX III fusion protein PBI. PBI is used to stimulate lymphocyte proliferative
XX response in HTLV-III infected humans. It is suggested that PBI can be
XX used in the diagnosis, prophylaxis or therapy of AIDS. (Updated on 10-MAR
XX -2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF
XX field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 536 BP; 218 A; 86 C; 106 G; 126 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 108; DB 1; Length 536;
XX Best Local Similarity 100.0%; Pred. No. 1e-21;
XX Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TGTACAGACCCCAACAATACAGAAAAGTATCCGTATCCAGAGGACCGAGGAGA 60
XX 25 TGTACAGACCCCAACAATACAGAAAAGTATCCGTATCCAGAGGACCGAGGAGA 84
XX
XX 61 GCATTGTGTACATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
XX 85 GCATTGTGTACATAGGAAAATAGGAAATATGAGACAAGCACATTGT 132
XX
XX RESULT 8
XX AAN90626
XX ID AAN90626 standard; DNA; 536 BP.
XX
XX AC AAN90626;
XX
XX 24-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 22-JUN-1990 (first entry)
XX
XX DE N-terminal region of PBI.
XX
XX HIV; AIDS; env gene; HIV vaccine; ds.
XX
XX Simian-Human immunodeficiency virus.
XX
XX EP306219-A.
XX

```

PD 08-MAR-1989.
 XX
 PF 25-AUG-1988; 88EP-00307889.
 XX
 PR 27-AUG-1987; 87US-00090080.
 XX
 PA (REPK) REPLIGEN CORP.
 XX
 PI Busche JR, Putney SD, Jayaheerian K, Farley J, Grimailla R, Lynn D;
 PI Petro J, Okeiffe T;
 XX
 DR WPI; 1989-070387/10.
 XX
 PT New HIV proteins and peptide(s) - used in diagnosis, prophylaxis or
 PT therapy of AIDS, esp. for prepn. of vaccines against HIV infection.
 XX
 PS Disclosure; Page ?; 29pp; English.
 XX
 CC Protein derivative stimulates a lymphocyte proliferative response in HIV-
 CC infected humans, providing a means of diagnosis, protection and
 CC therapeutic value. Synthetic proteins AAP90278-83 are derived from this
 CC sequence. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
 CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
 CC field)
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 Best Local Similarity 100.0%; Pred. No. 1e-21;
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 QY 61 GCATTGTGTACATAGGAAAATAGGAAATATGAGACAGCATTTGT 108
 DB 85 GCATTGTGTACATAGGAAAATAGGAAATATGAGACAGCATTTGT 132
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 AAN90739
 ID AAN90739 standard; DNA; 537 BP.
 XX
 AC AAN90739;
 XX
 DT 25-MAR-2003 (revised)
 DT 08-JUN-1990 (first entry)
 XX
 DE DNA encoding HIV portion of fusion protein PB1.
 XX
 KW HIV; pdeltaPB1; pd2PB1; transfer vector; immunoadsorbent;
 KW vaccine. env gene; HTLV-III; fusion protein PB1.
 XX
 OS Human immunodeficiency virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..537
 FT /*tag= a
 XX
 PN BP311228-A.
 XX
 PD 12-APR-1989.
 XX
 PF 25-MAR-1988; 88EP-00302695.
 XX
 PR 09-OCT-1987; 87US-00107703.
 XX
 PA (REPK) REPLIGEN CORP.
 XX
 PI Putney SD, Lynn D, Jayaheerian K, Mueller WT, Farley J;
 XX
 DR WPI; 1989-108200/15.

DR P-PSDB; AAP93537.
 XX
 PT Recombinant HIV proteins - used in assays for detecting and quantifying
 PT antibody against HIV and for incorporation into vaccine compns.
 XX
 PS Fig 2; Page ?; 17pp; English.
 XX
 CC It is an example of a nucleotide sequence coding for a novel protein
 CC which is composed of the HIV portion of fusion protein PB1, with or
 CC without the N-terminal Met. The novel protein is claimed and so are
 CC transfer vectors comprising AAN90740, eg plasmids pdeltaPB1 and pd2PB1.
 CC PB1 is disclosed in EPA 0255190. The novel protein can be used in assays
 CC for detecting or quantifying anti-HIV antibody and may be incorporated
 CC into vaccine compositions. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 537 BP; 218 A; 86 C; 106 G; 127 T; 0 U; 0 Other;
 Query Match 100.0%; Score 108; DB 1; Length 537;
 Best Local Similarity 100.0%; Pred. No. 1e-21;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTACAGACCCCAACAACTACACAAAGTATCCGTATCCAGAGGACGAGGAGA 60
 DB 28 TGTACAGACCCCAACAACTACACAAAGTATCCGTATCCAGAGGACGAGGAGA 87
 QY 61 GCATTGTGTACATAGGAAAATAGGAAATATGAGACAGCATTTGT 108
 DB 88 GCATTGTGTACATAGGAAAATAGGAAATATGAGACAGCATTTGT 135
 RESULT 10
 AAN92116
 ID AAN92116 standard; DNA; 537 BP.
 XX
 AC AAN92116;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 02-MAR-1990 (first entry)
 XX
 DE Polynucleotide encoding HIV portion of HTLV-III fusion protein PB1.
 XX
 KW HTLV-III envelope gene; HIV; pPB1; PB1;
 KW lymphocyte proliferative response; AIDS.
 XX
 OS Human lymphotropic virus typ.
 OS Chimeric.
 XX
 PN AU8821172-A.
 XX
 PD 13-APR-1989.
 XX
 PF 18-AUG-1988; 88AU-00021172.
 XX
 PR 09-OCT-1987; 87US-00107231.
 XX
 PA (REPK) REPLIGEN CORP.
 XX
 PI Putney SD, Lynn D, Jayaheerian K, Mueller WT, Farley J;
 XX
 DR WPI; 1989-157957/22.
 DR P-PSDB; AAP92014.
 XX
 PT Recombinant human T-cell leukaemia virus 3 proteins - used for
 PT stimulating lymphocyte proliferative response and in diagnosis
 PT prophylaxis or therapy of AIDS.
 XX
 PS Table 13A; Page ?; 85pp; English.
 XX
 CC It encodes the HIV portion of HTLV-III fusion protein PB1. PB1 is
 CC produced from plasmid pPB1 which contains the HTLV-III env gene from Pru
 CC II - Bgl II. the protein encoded by this polynucleotide is used to
 CC stimulate lymphocyte proliferative response in HTLV-III infected humans.

CC It is suggested that this protein can be used in the diagnosis,
 CC prophylaxis or therapy of AIDS and for the preparation of vaccines
 CC against HTLV-III. (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PA field.)

XX SQ Sequence 537 BP; 218 A; 86 C; 106 G; 127 T; 0 U; 0 Other;
 Query Match 100.0%; Score 108; DB 1; Length 537;
 Best Local Similarity 100.0%; Pred. No. 1.1e-21;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGAGCCCAACAAATACAGAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
 DB 28 TGTACAGAGCCCAACAAATACAGAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 87

QY 61 GCATTTGTTTACATAGGAAAATAGGAAAATATGAGACAAGCACATTGT 108
 DB 88 GCATTTGTTTACATAGGAAAATAGGAAAATATGAGACAAGCACATTGT 135

RESULT 11

AAN81450
 ID AAN81450 standard; DNA; 702 BP.

XX AC AAN81450;

XX DT 27-AUG-2003 (revised)
 XX DT 25-MAR-2003 (revised)
 XX DT 06-DEC-1990 (first entry)

XX DE Sequence encoding fusion protein PB1 of HTLV-III envelope protein.

XX KW Immunoassay; AIDS vaccine; antigen; immunogen; diagnostic; HIV; LAV; ds.

XX OS Human T-cell Lymphotropic virus type 3.

XX FH Key Location/Qualifiers
 XX FT CDS 1..702
 XX FT /*tag= a

XX PN EP255190-A.

XX PD 03-FEB-1988.

XX PF 19-JAN-1987; 87EP-00300397.

XX PR 01-AUG-1986; 86US-00892680.

XX PA (REPK) REPLIGEN CORP.

XX PI Putney SD, Lynn D, Javaherian K, Mueller W, Farley J;

XX DR WPI; 1988-030421/05.

XX DR P-PSDB; AAP81143.

XX PT New fragments of HTLV-III envelope protein - useful in antibody detection
 XX PT and vaccines, and new DNA coding sequences.

XX PS Claim 12; Page 63; 84pp; English.

XX CC Recombinant DNA transfer vectors which comprise all or part of the
 CC nucleotide sequence or equiv. contg. bases whose translated region codes
 CC for the R10, PB1, 590 or KH1 fragments of HTLV-III envelope protein. Host
 CC cells transformed with these vectors and HTLV-III envelope protein
 CC fragments R10, PB1, 590 and KH1 are claimed. These protein fragments are
 CC useful in immunoassays for detection of HTLV-III antibodies; as antigenic
 CC components of AIDS vaccines; also to stimulate lymphocyte proliferative
 CC response in infected individuals. (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-
 CC 2003 to correct OS field.)

XX SQ Sequence 702 BP; 260 A; 129 C; 148 G; 165 T; 0 U; 0 Other;

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 Best Local Similarity 100.0%; Pred. No. 1.1e-21;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGAGCCCAACAAATACAGAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
 DB 115 TGTACAGAGCCCAACAAATACAGAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 174

QY 61 GCATTTGTTTACATAGGAAAATAGGAAAATATGAGACAAGCACATTGT 108

DB 175 GCATTTGTTTACATAGGAAAATAGGAAAATATGAGACAAGCACATTGT 222

RESULT 12

AAN92112

ID AAN92112 standard; DNA; 702 BP.

XX AC AAN92112;

XX DT 25-MAR-2003 (revised)

XX DT 10-MAR-2003 (revised)

XX DT 02-MAR-1990 (first entry)

XX DE Polynucleotide encoding HTLV-III fusion protein PB1.

XX KW HTLV-III envelope gene; pPB1; PB1; lymphocyte proliferative response;
 XX KW AIDS.

XX OS Human lymphotropic virus typ.

XX OS Unidentified.

XX OS Chimeric.

XX PN AU8821172-A.

XX PD 13-APR-1989.

XX PF 18-AUG-1988; 88AU-00021172.

XX PR 09-OCT-1987; 87US-00107231.

XX PA (REPK) REPLIGEN CORP.

XX PI Putney SD, Lynn D, Javaherian K, Mueller WT, Farley J;

XX DR WPI; 1989-157957/22.

XX DR P-PSDB; AAP92010.

XX PT Recombinant human T-cell leukaemia virus 3 proteins - used for
 XX PT stimulating lymphocyte proliferative response and in diagnosis
 XX PT prophylaxis or therapy of AIDS.

XX PS Table 9A; Page ?; 85pp; English.

XX CC It encodes a protein called PB1 (26kD) which is an HTLV fusion protein
 CC produced from pPB1. pPB1 contains the HTLV-III env gene from Pvu II - Bgl
 CC II. The HIV portion of PB1 is used to stimulate lymphocyte proliferative
 CC response in HTLV-III infected humans. It is suggested that the HIV
 CC portion can be used in the diagnosis, prophylaxis or therapy of AIDS and
 CC for the preparation of vaccines against HTLV-III. (Updated on 10-MAR-2003
 CC to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 702 BP; 260 A; 129 C; 148 G; 165 T; 0 U; 0 Other;

Query Match 100.0%; Score 108; DB 1; Length 702;
 Best Local Similarity 100.0%; Pred. No. 1.1e-21;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGAGCCCAACAAATACAGAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60

DB 115 TGTACAGAGCCCAACAAATACAGAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 174

QY 61 GCATTGTTTACATAGGAAAAATAGGAAATATGAGCAACGACATTGT 108
 Db 175 GCATTGTTTACATAGGAAAAATAGGAAATATGAGCAACGACATTGT 222

RESULT 13

AAQ35897
 ID AAQ35897 standard; DNA; 702 BP.
 AC AAQ35897;
 XX
 XX 25-MAR-2003 (revised)
 DT 02-JUN-1993 (first entry)
 XX
 XX Recombinant PBI fusion protein gene.
 XX
 XX Human immunodeficiency virus; HIV; envelope protein; AIDS; ds.
 XX
 XX Synthetic.
 OS
 XX EP525828-A2.
 PN
 XX
 XX 03-FEB-1993.
 PD
 XX
 XX 19-JAN-1987; 92EP-00116879.
 PF
 XX
 XX 01-AUG-1986; 86US-00892680.
 PR
 XX
 XX (REPK) REPLIGEN CORP.
 PA

Putney SD, Lynn D, Javaherian K, Mueller WT, Farley J;
 WPI; 1993-038178/05.
 P-PSDB; AAR31943.

XX
 XX New recombinant HIV envelope protein PBI - for treatment, prevention and
 PT diagnosis of HIV and AIDS.
 PT
 PS
 XX Claim 4; Page 12; 18pp; English.

XX
 XX The DNA sequence contains essentially the HIV env gene from the PvuII

CC site to BglII site and encodes a novel recombinant HIV envelope protein,
 CC PBI. This plasmid in a suitable host, E. coli, can be used to produce the
 CC HIV 26kD fusion protein PBI. The protein can be used in diagnosis (in
 CC immunochemical assays, as an immuno- adsorbant), prophylaxis (a vaccine)
 CC or therapy of AIDS. Fragments of PBI can be used to stimulate a
 CC lymphocyte proliferative response in HIV-infected humans. This would then
 CC stimulate the immune system to respond to HIV. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC

SQ Sequence 702 BP; 260 A; 129 C; 148 G; 165 T; 0 U; 0 Other;

Query Match 100.0%; Score 108; DB 2; Length 702;
 Best Local Similarity 100.0%; Pred. No. 1.1e-21;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACAGACCCCAACACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
 Db 115 TGTCACAGACCCCAACACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 174

QY 61 GCATTGTTTACATAGGAAAAATAGGAAATATGAGCAACGACATTGT 108

Db 175 GCATTGTTTACATAGGAAAAATAGGAAATATGAGCAACGACATTGT 222

RESULT 14

AA92109
 ID AA92109 standard; DNA; 1056 BP.
 AC AA92109;
 XX

XX 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)

DT 02-MAR-1990 (first entry)

XX Synthetic polynucleotide encoding HTLV-III gp160 envelope protein.

XX HTLV-III envelope protein gp160; p590; p590; 590;

KW Lymphocyte proliferative response; AIDS.

OS Synthetic.

XX AU8821172-A.

PN 13-APR-1989.

XX 18-AUG-1988; 88AU-00021172.

PF 09-OCT-1987; 87US-00107231.

XX (REPK) REPLIGEN CORP.

XX Putney SD, Lynn D, Javaherian K, Mueller WT, Farley J;

XX WPI; 1989-157957/22.

XX Recombinant human T-cell leukaemia virus 3 proteins - used for

PT stimulating lymphocyte proliferative response and in diagnosis

PT prophylaxis or therapy of AIDS.

XX Example 6; Table 6; 85pp; English.

XX It is a synthetic fragment which encodes a portion of HTLV-III gp160

CC envelope protein. It has a blunt end on the 5' end and a TCGA overhang on

CC the non-coding strand at the 3' end which will ligate with HindIII. Used

CC in example to construct p590 which is used to express recombinant HTLV-

CC III fusion protein 590. 590 is used to stimulate lymphocyte proliferative

CC response in HTLV-III infected humans. It is suggested that 590 can be

CC used in the diagnosis, prophylaxis or therapy of AIDS. (Updated on 10-MAR

CC -2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF

CC field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1056 BP; 384 A; 177 C; 255 G; 240 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 108; DB 1; Length 1056;

Best Local Similarity 100.0%; Pred. No. 1.1e-21;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACAGACCCCAACACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60

Db 25 TGTCACAGACCCCAACACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 84

QY 61 GCATTGTTTACATAGGAAAAATAGGAAATATGAGCAACGACATTGT 108

Db 85 GCATTGTTTACATAGGAAAAATAGGAAATATGAGCAACGACATTGT 132

RESULT 15

AA90740

ID AA90740 standard; DNA; 1059 BP.

XX

AC AA90740;

XX

DT 25-MAR-2003 (revised)

DT 08-JUN-1990 (first entry)

XX

DE DNA encoding HIV portion of fusion protein 590.

XX HIV; p590; pdeltaPBI; pd2PBI; transfer vector; immunoadsorbent;

KW vaccine. env gene; HTLV-III; fusion protein 590.

XX

OS Human immunodeficiency virus.

XX

Key Location/Qualifiers

1..1059

/*tag= a

FT CDS

FT


```

XX EP311228-A.
PN
XX
XX 12-APR-1989.
PD
XX
XX 25-MAR-1988; 88EP-00302695.
PF
XX
XX 09-OCT-1987; 87US-00107703.
PR
XX
XX (REPK ) REPLIGEN CORP.
PA
XX
XX Putney SD, Lynn D, Javaherian K, Mueller WT, Farley J;
PI
XX
XX WPI: 1989-108200/15.
DR
XX
XX P-PSDB; AAP93538.
DR
XX
XX Recombinant HIV proteins - used in assays for detecting and quantifying
PT antibody against HIV and for incorporation into vaccine compns.
PT
XX
XX Fig 3; Page ?; 17pp; English.
PS
XX
XX It is an example of a nucleotide sequence coding for a novel protein
CC which is composed of the HIV portion of fusion protein 590, with or
CC without the N-terminal Met. The novel protein is claimed and so are
CC transfer vectors comprising AAN90740, eg plasmids pdeltaPB1 and pd2PB1.
CC 590 is disclosed in EPA 0255190. The novel protein can be used in assays
CC for detecting or quantifying anti-HIV antibody and may be incorporated
CC into vaccine compositions. (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
XX Sequence 1059 BP; 384 A; 180 C; 255 G; 240 T; 0 U; 0 Other;
SQ
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Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGTACAAGACCCCAACAATACAAAGAAAGTATCCGTATCCAGAGAGGACCAGGAGA 60
Db 28 TGTACAAGACCCCAACAATACAAAGAAAGTATCCGTATCCAGAGAGGACCAGGAGA 87
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Db 88 GCATTGTGTACAATAGGAAATAGGAAATATGAGACACACATTGT 135

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GenCore version 5.1.6
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Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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1	108	100.0	2945	6	Patent No. 5462872
2	108	100.0	8932	3	US-09-124-900-1
3	108	100.0	8933	3	US-08-463-210-4
4	108	100.0	8933	3	US-09-620-958A-3
5	108	100.0	8933	3	US-09-620-958A-4
6	108	100.0	8933	3	US-09-620-958A-9
7	108	100.0	8933	4	US-08-463-028-4
8	106.4	98.5	781	2	US-08-459-818-18
9	106.4	98.5	781	2	US-08-889-666-18
10	106.4	98.5	781	2	US-08-465-078-18
11	106.4	98.5	781	2	US-08-725-776-18
12	106.4	98.5	781	2	US-08-488-062-18
13	106.4	98.5	1497	2	US-07-916-098A-3
14	106.4	98.5	1568	1	US-08-589-446-7
15	106.4	98.5	1568	1	US-08-444-882-7
16	106.4	98.5	1568	3	US-08-389-459A-7
17	106.4	98.5	1568	3	US-08-987-867A-7
18	106.4	98.5	1571	2	US-08-037-816A-25
19	106.4	98.5	1571	2	US-08-530-146-25
20	106.4	98.5	2531	3	US-07-956-483-18
21	106.4	98.5	2571	2	US-07-916-098A-1
22	106.4	98.5	2644	3	US-08-472-240A-9
23	106.4	98.5	2694	1	US-08-147-890-1
24	106.4	98.5	3084	1	US-08-147-890-2
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31 106.4 98.5 9709 4 US-09-718-096-15 Sequence 15, Appli
32 106.4 98.5 9719 4 US-09-700-304-1 Sequence 1, Appli
33 106.4 98.5 12479 4 US-09-318-138-13 Sequence 13, Appli
34 106.4 98.5 12494 3 US-08-935-312-13 Sequence 13, Appli
35 106.4 98.5 12494 3 US-08-848-760B-33 Sequence 33, Appli
36 106.4 98.5 15581 3 US-08-646-538-33 Sequence 35, Appli
37 106.4 98.5 15581 3 US-09-503-222-35 Sequence 35, Appli
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42 101.6 94.1 2184 4 US-09-337-387-4 Sequence 4, Appli
43 65.2 60.4 9207 3 US-08-388-353-800 Sequence 800, App
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45 62 57.4 1763 4 US-09-646-028-43 Sequence 43, Appli

ALIGNMENTS

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; Patent No. 5462872

; APPLICANT: Jonak, Zdenka L.; Debouck, Christine; Clark, Robert

; Trulli, Stephen

; TITLE OF INVENTION: HUMAN LYMPHOID CELLS EXPRESSING HUMAN

; IMMUNODEFICIENCY VIRUS ENVELOPE PROTEIN GP160

; NUMBER OF SEQUENCES: 1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/134,128

; FILING DATE: 08-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 906,613

; FILING DATE: 30-JUN-1992

; APPLICATION NUMBER: 587,011

; FILING DATE: 24-SEP-1990

; SEQ ID NO:1:

; LENGTH: 2945

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Matches 108; Conservative 0;

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Db 1213 GCATTGTGTACATAGGAAAAATAGGAATATGAGCAAGCATTGT 1260

RESULT 2

US-09-124-900-1

; Sequence 1, Application US/09124900

; Patent No. 6268484

; GENERAL INFORMATION:

; APPLICANT: KATINGER, Hermann

; APPLICANT: BUCHACHER, Andrea

; APPLICANT: ERNST, Wolfgang

; APPLICANT: BALLAUN, Claudia

; APPLICANT: FURTSCHER, Martin

; APPLICANT: TRKOLA, Alexandra

; APPLICANT: PREDL, Renate

; APPLICANT: SCHWATZ, Christine

; APPLICANT: KLIMA, Annelies

; APPLICANT: STEINDL, Franz

; APPLICANT: MUSTER, Thomas

; TITLE OF INVENTION: HIV-Vaccines

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? ORIGINAL SOURCE:
? ORGANISM: HTLV-III
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 1..8933
? OTHER INFORMATION: /standard name= "Clone BH10"
? OTHER INFORMATION: /note= "Corresponds to nucleotide positions 222 to
? OTHER INFORMATION: 9154 in figure 3 of EP 85307260"
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 113..1648
? OTHER INFORMATION: /product= "gag"
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 1408..4452
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? NAME/KEY: mat_peptide
? LOCATION: 4367..4975
? OTHER INFORMATION: /product= "sor"
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 5560..8148
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?
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Query Match 100.0%; Score 108; DB 3; Length 8933;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db TGTACAAGACCCCAACAACAATACAGAAAAAGTATCCGTATCCAGAGAGACCAAGGAGA 6525

QY 61 GCATTTGTTACATAGCAAAAAATAGGAATATAGACAAGCACATTGT 108
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Db 6526 GCATTTGTTACATAGCAAAAAATAGGAATATAGACAAGCACATTGT 6573

RESULT 4
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; Sequence 3, Application US/09620958A
; Patent No. 6294338
; GENERAL INFORMATION:
; APPLICANT: Nunomura, Kiyotada
; TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
; FILE REFERENCE: GP104-02.UT
; CURRENT APPLICATION NUMBER: US/09/620,958A
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8933
; TYPE: RNA
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)...(8933)
; OTHER INFORMATION: Sequence of transcripts produced from the BH10
; Patent No. 6294338
; OTHER INFORMATION: plasmid.
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Query Match 100.0%; Score 108; DB 3; Length 8933;
Best Local Similarity 82.4%; Pred. No. 2.5e-24;
Matches 89; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAAGACCCCAACAACAATACAGAAAAAGTATCCGTATCCAGAGAGACCAAGGAGA 60
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Db 6466 UGUACAAGACCCCAACAACAATACAGAAAAAGTATCCGTATCCAGAGAGACCAAGGAGA 6525

QY 61 GCATTTGTTACATAGCAAAAAATAGGAATATAGACAAGCACATTGT 108
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Db 6526 GCAUUGUUAUAGGAAAAAUAUGAGAAUUAUGAGACACACAUUGU 6573

RESULT 5

US-09-620-958A-4

; Sequence 4, Application US/09620958A
; Patent No. 6294338
; GENERAL INFORMATION:
; APPLICANT: Nunomura, Kiyotada
; TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
; FILE REFERENCE: GP104-02.UT
; CURRENT APPLICATION NUMBER: US/09/620,958A
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 8933
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the IAC-Asrc pseudo target
; Patent No. 6294338
; NAME/KEY: mutation
; LOCATION: (4135)...(4155)
; OTHER INFORMATION: Mutated positions: 4135, 4140-1, 4145, 4150,
; OTHER INFORMATION: 4152-3, 4155
US-09-620-958A-4

Query Match 100.0%; Score 108; DB 3; Length 8933;
Best Local Similarity 82.4%; Pred. No. 2.5e-24;
Matches 89; Conservative 19; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTACAGACCCCAACAACATCAAGAAAAAGTATCCGTATCCAGAGAGGACCGGAGA 60
Db 6466 UGUACAGACCCCAACAACAUACAAGAAAAAGUACCGUACAGAGGACCGGAGA 6525

QY 61 GCATTGTTCATAGGAAAAATAGAAATATGACAGACGACATTGT 108

Db 6526 GCAUUGUUAUAGGAAAAAUAUGAGAAUUAUGAGACACACAUUGU 6573

RESULT 6

US-09-620-958A-9

; Sequence 9, Application US/09620958A
; Patent No. 6294338
; GENERAL INFORMATION:
; APPLICANT: Nunomura, Kiyotada
; TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
; FILE REFERENCE: GP104-02.UT
; CURRENT APPLICATION NUMBER: US/09/620,958A
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 8933
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the IAC-Bsrc pseudo target
; Patent No. 6294338
; NAME/KEY: mutation
; LOCATION: (4140)...(4159)
; OTHER INFORMATION: Mutated positions: 4140-42, 4145-47, 4152,
; OTHER INFORMATION: 4156-57, 4159
US-09-620-958A-9

Query Match 100.0%; Score 108; DB 3; Length 8933;
Best Local Similarity 82.4%; Pred. No. 2.5e-24;
Matches 89; Conservative 19; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTACAGACCCCAACAACATCAAGAAAAAGTATCCGTATCCAGAGAGGACCGGAGA 60
Db 6466 UGUACAGACCCCAACAACAUACAAGAAAAAGUACCGUACAGAGGACCGGAGA 6525

QY 61 GCATTGTTCATAGGAAAAATAGAAATATGACAGACGACATTGT 108
Db 6526 GCAUUGUUAUAGGAAAAAUAUGAGAAUUAUGAGACACACAUUGU 6573

RESULT 7

US-08-463-028-4
; Sequence 4, Application US/08463028
; Patent No. 6610476
; GENERAL INFORMATION:
; APPLICANT: CHANG, Nancy T.
; APPLICANT: GALLO, Robert C.
; APPLICANT: WONG-STAL, Flossie
; TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,028
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/693,866
; FILING DATE: 23-JAN-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/659,339
; FILING DATE: 10-OCT-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Serunian, Leslie A.
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4193US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8933 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: HTLV-III
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..8933
; OTHER INFORMATION: /standard_name= "Clone BH10"
; OTHER INFORMATION: /note= "Corresponds to nucleotide positions 222 to
; OTHER INFORMATION: 9154 in figure 3 of EP 85307260"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 113..1648
; OTHER INFORMATION: /product= "gag"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1408..14452
; OTHER INFORMATION: /product= "pol"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 4367..4975
; OTHER INFORMATION: /product= "sor"

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; FEATURE:
; NAME/KEY: mat.peptide
; LOCATION: 5560..8148
; OTHER INFORMATION: /product="env"
US-08-463-028-4

Query Match 100.0%; Score 108; DB 4; Length 8933;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
Db 6466 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 6525

QY 61 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 108
Db 6526 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 6573

RESULT 8
US-08-459-818-18
; Sequence 18, Application US/08459818
; Patent No. 5851795
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,818
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.35US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-459-818-18

Query Match 98.5%; Score 106.4; DB 2; Length 781;
Best Local Similarity 99.1%; Pred. No. 4.2e-24;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
Db 563 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 622

QY 61 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 108
Db 623 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 670

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; FEATURE:
; NAME/KEY: mat.peptide
; LOCATION: 5560..8148
; OTHER INFORMATION: /product="env"
US-08-463-028-4

Query Match 100.0%; Score 108; DB 4; Length 8933;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
Db 6466 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 6525

QY 61 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 108
Db 6526 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 6573

RESULT 9
US-08-889-666-18
; Sequence 18, Application US/08889666
; Patent No. 5885796
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,666
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-889-666-18

Query Match 98.5%; Score 106.4; DB 2; Length 781;
Best Local Similarity 99.1%; Pred. No. 4.2e-24;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
Db 563 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 622

QY 61 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 108
Db 623 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 670

;
; FEATURE:
; NAME/KEY: mat.peptide
; LOCATION: 5560..8148
; OTHER INFORMATION: /product="env"
US-08-463-028-4

Query Match 100.0%; Score 108; DB 4; Length 8933;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
Db 6466 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 6525

QY 61 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 108
Db 6526 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 6573

RESULT 10
US-08-465-078-18
; Sequence 18, Application US/08465078
; Patent No. 5885796
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,666
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-889-666-18

Query Match 98.5%; Score 106.4; DB 2; Length 781;
Best Local Similarity 99.1%; Pred. No. 4.2e-24;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
Db 563 TGTACAGACCCCAACAACATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 622

QY 61 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 108
Db 623 GCATTGTGTACATAGGAAAAATAGGAATATGAGACAAGCACATTGT 670
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RESULT 11
US-08-725-776-18
; Sequence 18, Application US/08725776
; Patent No. 5968510
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTIA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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1 SOFTWARE: PatentIn Release #1.0, Version #1.30
2 CURRENT APPLICATION DATA:
3 APPLICATION NUMBER: US/08/725,776
4 FILING DATE:
5 CLASSIFICATION:
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 08/375390
8 FILING DATE: 18-JAN-1995
9 ATTORNEY/AGENT INFORMATION:
10 NAME: Adriano, Sarah B.
11 REGISTRATION NUMBER: 34,470
12 REFERENCE/DOCKET NUMBER: 30436-35US01
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: 310-445-1140
15 TELEFAX: 310-445-9031
16 INFORMATION FOR SEQ ID NO: 18:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 781 base pairs
19 TYPE: nucleic acid
20 STRANDEDNESS: single
21 TOPOLOGY: linear
22 MOLECULE TYPE: DNA (genomic)
23 US-08-725-776-18
24
25 Query Match 98.5%; Score 106.4; DB 2;
26 Best Local Similarity 99.1%; Pred. No. 4.2e-24;
27 Matches 107; Conservative 0; Mismatches 1;
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29 QY 1 TGTACAAGACCCCAACAACAATAACAAGAAAAAGTATCCGTA
30 Db 563 TGTACAAGACCCCAACAACAATAACAAGAAAAAGTATCCGTA
31
32 QY 61 GCATTGTGTACAATAGGAAAAATAGGAATATATGAGACAAG
33 Db 623 GCATTGTGTACAATAGGAAAAATAGGAATATATGAGACAAG
34
35 RESULT 12
36 US-08-488-062-18
37 Sequence 18, Application US/08488062
38 Patent No. 5977318
39
40 GENERAL INFORMATION:
41 APPLICANT: Linsley, Peter S.
42 APPLICANT: Ledbetter, Jeffrey A.
43 APPLICANT: Damle, Nitin K.
44 APPLICANT: Brady, William
45 APPLICANT: Kiener, Peter A.
46 TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
47 NUMBER OF SEQUENCES: 26
48 CORRESPONDENCE ADDRESS:
49 ADDRESSEE: Merchant & Gould
50 CITY: Los Angeles
51 STATE: California
52 COUNTRY: USA
53 ZIP: 90025
54
55 COMPUTER READABLE FORM:
56 MEDIUM TYPE: Floppy disk
57 COMPUTER: IBM PC compatible
58 OPERATING SYSTEM: PC-DOS/MS-DOS
59 SOFTWARE: PatentIn Release #1.0, Version #1.30
60 CURRENT APPLICATION DATA:
61 APPLICATION NUMBER: US/08/488,062
62 FILING DATE: 07-JUN-1995
63 CLASSIFICATION: 435
64 PRIOR APPLICATION DATA:
65 APPLICATION NUMBER: US 08/375390
66 FILING DATE: 18-JAN-1995
67 ATTORNEY/AGENT INFORMATION:
68 NAME: Adriano, Sarah B.
69 REGISTRATION NUMBER: 34,470
70 REFERENCE/DOCKET NUMBER: 30436-35US01
71 TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-489-062-18

Query Match          98.5%; Score 106.4; DB 2; Length 781;
Best Local Similarity 99.1%; Pred. No. 4.2e-24;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTACAGACCCCAACAATACAGAAAAGTATCCGTATCCAGAGAGGACGAGGAGA 60
Db 563 TGTACAGACCCCAACAATACAGAAAAGTATCCGTATCCAGAGAGGACGAGGAGA 622
QY 61 GCATTGTTCATAGGAAAATAGGAAAATATGAGACAAGCACATTGT 108
Db 623 GCATTGTTCATAGGAAAATAGGAAAATATGAGACAAGCACATTGT 670

RESULT 13
US-07-916-098A-3
; Sequence 3, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916.098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1497 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-489-062-18

Query Match          98.5%; Score 106.4; DB 2; Length 1497;
Best Local Similarity 99.1%; Pred. No. 5e-24;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTACAGACCCCAACAATACAGAAAAGTATCCGTATCCAGAGAGGACGAGGAGA 60
Db 874 TGTACAGACCCCAACAATACAGAAAAGTATCCGTATCCAGAGAGGACGAGGAGA 933
QY 61 GCATTGTTCATAGGAAAATAGGAAAATATGAGACAAGCACATTGT 108
Db 934 GCATTGTTCATAGGAAAATAGGAAAATATGAGACAAGCACATTGT 981

RESULT 14
US-08-589-446-7
; Sequence 7, Application US/08589446
; Patent No. 5614413
; GENERAL INFORMATION:
; APPLICANT: MORROW, CASEY D.
; TITLE OF INVENTION: ENCAPSIDATED POLIOVIRUS NUCLEIC
; TITLE OF INVENTION: ACID AND METHODS OF MAKING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,446
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,009
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Geary III, William C.
; REGISTRATION NUMBER: 31,359
; REFERENCE/DOCKET NUMBER: UAG-004
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..1565
US-08-589-446-7
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Search completed: March 11, 2004, 23:12:13
Job time : 59.4954 secs

Query Match	98.5%	Score 106.4	DB 1	Length 1568
Best Local Similarity	99.1%	Pred. No. 5.1e-24		
Matches 107	Conservative 0	Mismatches 1	Indels 0	Gaps 0

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QY	61	GCATTTGTTTCAATAGGAAAAAATAGGAAATATGACAAGCACATTGT	108
Db	340	GCATTTGTTTCAATAGGAAAAAATAGGAAATATGACAAGCACATTGT	387

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 20:30:23 ; Search time 65,0917 Seconds
(without alignments)
1099.812 Million cell updates/sec

Title: US-10-003-035-75

Perfect score: 129

Sequence: 1 ttattcataatgatagtagg.....acctcccaatcccgaggaggga 129

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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5: /cgn2_6/prodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	2945	6	Patent No. 5462872
2	129	100.0	8932	3	Sequence 1, Appli
3	129	100.0	8933	3	Sequence 4, Appli
4	129	100.0	8933	3	Sequence 3, Appli
5	129	100.0	8933	3	Sequence 4, Appli
6	129	100.0	8933	3	Sequence 9, Appli
7	129	100.0	8933	4	Sequence 4, Appli
8	127.4	98.8	1596	3	Sequence 651, App
9	127.4	98.8	1596	3	Sequence 651, App
10	127.4	98.8	2696	4	Sequence 1, Appli
11	127.4	98.8	2730	3	Sequence 1, Appli
12	127.4	98.8	2940	2	Sequence 3, Appli
13	127.4	98.8	3426	2	Sequence 2, Appli
14	127.4	98.8	3480	2	Sequence 4, Appli
15	127.4	98.8	3721	2	Sequence 5, Appli
16	127.4	98.8	3993	2	Sequence 6, Appli
17	127.4	98.8	4059	2	Sequence 7, Appli
18	127.4	98.8	4632	2	Sequence 8, Appli
19	127.4	98.8	7399	2	Sequence 9, Appli
20	127.4	98.8	9709	2	Sequence 5, Appli
21	127.4	98.8	9709	3	Sequence 1, Appli
22	127.4	98.8	9709	3	Sequence 1, Appli
23	127.4	98.8	9709	4	Sequence 15, Appl
24	127.4	98.8	9709	4	Sequence 15, Appl
25	127.4	98.8	12479	4	Sequence 13, Appl
26	127.4	98.8	12494	3	Sequence 13, Appl
27	127.4	98.8	12494	3	Sequence 33, Appl

28 127.4 98.8 15981 3 US-08-646-538-35 Sequence 35, Appli
29 127.4 98.8 15581 3 US-09-503-222-35 Sequence 35, Appli
30 125.8 97.5 1260 1 US-08-467-933-7 Sequence 7, Appli
31 125.8 97.5 1451 1 US-07-924-028A-1 Sequence 1, Appli
32 125.8 97.5 2571 2 US-07-916-098A-1 Sequence 1, Appli
33 125.8 97.5 2694 1 US-08-147-890-1 Sequence 2, Appli
34 125.8 97.5 3084 1 US-08-147-890-2 Sequence 6, Appli
35 125.8 97.5 3563 3 US-08-463-210-6 Sequence 6, Appli
36 125.8 97.5 3563 4 US-08-463-028-6 Sequence 1, Appli
37 125.8 97.5 9719 4 US-09-700-304-1 Sequence 1, Appli
38 121.8 94.4 1568 1 US-08-589-446-7 Sequence 7, Appli
39 121.8 94.4 1568 1 US-08-444-882-7 Sequence 7, Appli
40 121.8 94.4 1568 1 US-08-389-459A-7 Sequence 7, Appli
41 121.8 94.4 1568 3 US-08-987-867A-7 Sequence 7, Appli
42 117.8 91.3 1208 3 US-08-388-353-615 Sequence 615, App
43 117.8 91.3 1208 3 US-08-488-551B-615 Sequence 615, App
44 117.8 91.3 9207 3 US-08-388-353-800 Sequence 800, App
45 117.8 91.3 9207 3 US-08-488-551B-800 Sequence 800, App

ALIGNMENTS

RESULT 1

5462872-1

; Patent No. 5462872

; APPLICANT: Jonak, Zdenka L.; Debouck, Christine; Clark, Robert

; Trulli, Stephen

; TITLE OF INVENTION: HUMAN LYMPHOID CELLS EXPRESSING HUMAN

; IMMUNODEFICIENCY VIRUS ENVELOPE PROTEIN GP160

; NUMBER OF SEQUENCES: 1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/134,128

; FILING DATE: 08-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 906,613

; FILING DATE: 30-JUN-1992

; APPLICATION NUMBER: 587,011

; FILING DATE: 24-SEP-1990

; SEQ ID NO:1:

; LENGTH: 2945

5462872-1

Query Match 100.0%; Score 129; DB 6; Length 2945;

Best Local Similarity 100.0%; Pred. No. 4e-33; 0; Gaps 0;

Matches 129; Conservative 0; Mismatches 0; Indels 0;

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Db 2317 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGAAATAGTTTCTGTACTTTCT 2376

QY 61 GTAGTCAATAGAGTTAGGAGGAGGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 120

Db 2377 GTAGTCAATAGAGTTAGGAGGAGGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 2436

QY 121 CCGAGGGGA 129

Db 2437 CCGAGGGGA 2445

RESULT 2

US-09-124-900-1

; Sequence 1, Application US/09124900

; Patent No. 6268484

; GENERAL INFORMATION:

; APPLICANT: KATINGER, Hermann

; APPLICANT: BUCHACHER, Andrea

; APPLICANT: ERNST, Wolfgang

; APPLICANT: BALLAUN, Claudia

; APPLICANT: PURTSCHER, Martin

; APPLICANT: TRKOLA, Alexandra

; APPLICANT: FREDL, Renate

; APPLICANT: SCHWATZ, Christine

```

; APPLICANT: KLIMA, Annelies
; APPLICANT: STEINDL, Franz
; APPLICANT: MUSTER, Thomas
; TITLE OF INVENTION: HIV-Vaccines
; FILE REFERENCE: 1939-112P
; CURRENT APPLICATION NUMBER: US/09/124,900
; CURRENT FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: PCT/EP95/01481
; PRIOR FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 8932
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-09-124-900-1

Query Match 100.0%; Score 129; DB 3; Length 8932;
Best Local Similarity 100.0%; Pred. No. 5.7e-33;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTCATATGATAGTAGGAGGCTTGGTAGGTTTAAGATAGTTTTGCTGTACTTTCT 60
Db 7629 TTATTCATATGATAGTAGGAGGCTTGGTAGGTTTAAGATAGTTTTGCTGTACTTTCT 7688

Qy 61 GTAGTGAATAGAGTTAGGACGGGATATTCACCATTCGTTTCAGACCCACTCCCAATC 120
Db 7689 GTAGTGAATAGAGTTAGGACGGGATATTCACCATTCGTTTCAGACCCACTCCCAATC 7748

Qy 121 CCGAGGGGA 129
Db 7749 CCGAGGGGA 7757

RESULT 3
US-08-463-210-4
; Sequence 4, Application US/08463210
; Patent No. 6001977
; GENERAL INFORMATION:
; APPLICANT: CHANG, Nancy T.
; APPLICANT: GALLO, Robert C.
; APPLICANT: WONG-STAAAL, Flossie
; TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,210
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/693,866
; FILING DATE: 23-JAN-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/659,339
; FILING DATE: 10-OCT-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Serunian, Leslie A.
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4193US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-4800
; TELEFAX: (212) 751-6849

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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8933 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: HTLV-III
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..8933
; OTHER INFORMATION: /standard name= "Clone BH10"
; OTHER INFORMATION: /note= "Corresponds to nucleotide positions 222 to
; OTHER INFORMATION: 9154 in figure 3 of EP 85307260"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 113..1648
; OTHER INFORMATION: /product= "gag"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1408..4452
; OTHER INFORMATION: /product= "pol"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 4367..4975
; OTHER INFORMATION: /product= "sor"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 5560..8148
; OTHER INFORMATION: /product= "env"
US-08-463-210-4

Query Match 100.0%; Score 129; DB 3; Length 8933;
Best Local Similarity 100.0%; Pred. No. 5.7e-33;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTCATATGATAGTAGGAGGCTTGGTAGGTTTAAGATAGTTTTGCTGTACTTTCT 60
Db 7630 TTATTCATATGATAGTAGGAGGCTTGGTAGGTTTAAGATAGTTTTGCTGTACTTTCT 7689

Qy 61 GTAGTGAATAGAGTTAGGACGGGATATTCACCATTCGTTTCAGACCCACTCCCAATC 120
Db 7690 GTAGTGAATAGAGTTAGGACGGGATATTCACCATTCGTTTCAGACCCACTCCCAATC 7749

Qy 121 CCGAGGGGA 129
Db 7750 CCGAGGGGA 7758

RESULT 4
US-09-620-958A-3
; Sequence 3, Application US/09620958A
; Patent No. 6294338
; GENERAL INFORMATION:
; APPLICANT: Nunomura, Kiyotada
; TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
; FILE REFERENCE: GP104-02 UT
; CURRENT APPLICATION NUMBER: US/09/620,958A
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8933
; TYPE: RNA
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)...(8933)
; OTHER INFORMATION: Sequence of transcripts produced from the BH10
; Patent No. 6294338
; OTHER INFORMATION: plasmid.

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HTLV-III
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..8933
OTHER INFORMATION: /standard name= "Clone BH10"
OTHER INFORMATION: /note= "Corresponds to nucleotide positions 222 to
OTHER INFORMATION: 9154 in figure 3 of EP 85307260"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 113..1648
OTHER INFORMATION: /product= "gag"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1408..4452
OTHER INFORMATION: /product= "pol"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 4367..4975
OTHER INFORMATION: /product= "sor"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 5560..8148
OTHER INFORMATION: /product= "env"
US-08-463-028-4

Query Match 100.0%; Score 129; DB 4; Length 8933;
Best Local Similarity 100.0%; Pred. No. 5.7e-33;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTCATATGATAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTGCTGTACTTTCT 60
DB 7630 TTATTCATATGATAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTGCTGTACTTTCT 7689

QY 61 GTAGTGAATAGATTAGGAGGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 120
DB 7690 GTAGTGAATAGATTAGGAGGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 7749

QY 121 CCGAGGGGA 129
DB 7750 CCGAGGGGA 7758

RESULT 8
US-08-388-353-651
; Sequence 651, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Leamont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:

FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 651:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-651

Query Match 98.8%; Score 127.4; DB 3; Length 1596;
Best Local Similarity 99.2%; Pred. No. 1.1e-32;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTATTCATATGATAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTGCTGTACTTTCT 60
DB 193 TTATTCATATGATAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTGCTGTACTTTCT 252

QY 61 GTAGTGAATAGATTAGGAGGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 120
DB 253 ATAGTGAATAGATTAGGAGGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 312

QY 121 CCGAGGGGA 129
DB 313 CCGAGGGGA 321

RESULT 9
US-08-488-551B-651
; Sequence 651, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 651:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1596 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-651

Query Match          98.8%; Score 127.4; DB 3; Length 1596;
Best Local Similarity 99.2%; Pred. No. 1.1e-32;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTATTCATAATGATAGTAGGAGGCTTGTTAGGTTTAAAGATAGTTTTTGCTGTACTTTCT 60
Db 193 TTATTCATAATGATAGTAGGAGGCTTGTTAGGTTTAAAGATAGTTTTTGCTGTACTTTCT 252

Qy 61 GTAGTGAATAGATTAGGCAGGAGTATTCACCATTCGTTTCAGACCCACTCCCAATC 120
Db 253 ATAGTGAATAGATTAGGCAGGAGTATTCACCATTCGTTTCAGACCCACTCCCAATC 312

Qy 121 CCGAGGGGA 129
Db 313 CCGAGGGGA 321

RESULT 10
US-09-325-131B-1
; Sequence 1, Application US/09325131B
; Patent No. 6492104
; GENERAL INFORMATION:
; APPLICANT: CLOYD, MILES W.
; APPLICANT: RAMSEY, KEITH
; TITLE OF INVENTION: BIA TEST USING NONDENATURED HIV ANTIGEN FOR EARLY
; TITLE OF INVENTION: DETECTION OF HIV INFECTION
; FILE REFERENCE: UTSG:234
; CURRENT APPLICATION NUMBER: US/09/325,131B
; CURRENT FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 08/728,122
; PRIOR FILING DATE: 1996-10-09
; PRIOR APPLICATION NUMBER: 08/143,168
; PRIOR FILING DATE: 1993-10-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2696
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-325-131B-1

Query Match          98.8%; Score 127.4; DB 4; Length 2696;
Best Local Similarity 99.2%; Pred. No. 1.3e-32;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2489 TTATTCATAATGATAGTAGGAGGCTTGTTAGGTTTAAAGATAGTTTTTGCTGTACTTTCT 2548

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Qy 121 CCGAGGGGA 129
Db 2609 CCGAGGGGA 2617

RESULT 11
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US-08-728-122-1
; Sequence 1, Application US/08728122
; Patent No. 6074646
; GENERAL INFORMATION:
; APPLICANT: Cloyd, Miles W.
; APPLICANT: Ramsey, Keith M.
; TITLE OF INVENTION: A New EIA Test Using No. 6074646-Denatured
; TITLE OF INVENTION: HIV Antigen for Early Detection of
; TITLE OF INVENTION: HIV Infection
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akin, Gump, Straus, Hauer & Feid, L.L.P.
; STREET: 816 Congress Avenue, Suite 1900
; CITY: Austin
; STATE: Texas
; COUNTRY: USA
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,122
; FILING DATE: 09-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: 43424.0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 499-6200
; TELEFAX: (512) 499-6290
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2730 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-728-122-1

Query Match          98.8%; Score 127.4; DB 3; Length 2730;
Best Local Similarity 99.2%; Pred. No. 1.3e-32;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTATTCATAATGATAGTAGGAGGCTTGTTAGGTTTAAAGATAGTTTTTGCTGTACTTTCT 60
Db 2519 TTATTCATAATGATAGTAGGAGGCTTGTTAGGTTTAAAGATAGTTTTTGCTGTACTTTCT 2578

Qy 61 GTAGTGAATAGATTAGGCAGGAGTATTCACCATTCGTTTCAGACCCACTCCCAATC 120
Db 2579 GTAGTGAATAGATTAGGCAGGAGTATTCACCATTCGTTTCAGACCCACTCCCAATC 2638

Qy 121 CCGAGGGGA 129
Db 2639 CCGAGGGGA 2647

RESULT 12
US-08-418-848A-3
; Sequence 3, Application US/08418848A
; Patent No. 5847096
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, MANFRED, HARMISON II.
; APPLICANT: GEORGE G., CHANG-JIE, CHEN, BANJERJEA, AKHIL
; TITLE OF INVENTION: DEFECTIVE, INTERFERING
; TITLE OF INVENTION: HIV PARTICLES
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; COUNTRY: U.S.A.
```

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; APPLICATION NUMBER: 07/936,849
; FILING DATE: 28-AUG-1992
; CLASSIFICATION: 526
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4091US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-418-848A-2

Query Match 98.8%; Score 127.4; DB 2; Length 3426;
Best Local Similarity 99.2%; Pred. No. 1.4e-32;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTATTCAATGATAGTAGGAGGCTTGAGGTTTAAGATAGTTTTGCTGTACTTTCT 60
Db 1981 TTATTCAATGATAGTAGGAGGCTTGAGGTTTAAGATAGTTTTGCTGTACTTTCT 2040

QY 61 GTAGTCAATAGAGTTAGGAGGAGGATATCCACCATTTATCGTTTCAGACCCCACTCCCAATC 120
Db 2041 ATAGTCAATAGAGTTAGGAGGAGGATATTCACCATTTATCGTTTCAGACCCCACTCCCAATC 2100

QY 121 CCGAGGGGA 129
Db 2101 CCGAGGGGA 2109

RESULT 14
US-08-418-848A-4
; Sequence 4, Application US/08418848A
; Patent No. 5847096
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, MANFRED, HARMISON II,
; APPLICANT: GEORGE G., CHANG-JIE, CHEN, BANJERJEA, AKHIL
; TITLE OF INVENTION: DEFECTIVE, INTERFERING
; TITLE OF INVENTION: HIV PARTICLES
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,848A
; FILING DATE: 07-APR-1995
; CLASSIFICATION: 526
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936,849
; FILING DATE: 28-AUG-1992
; CLASSIFICATION: 526
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4091US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; TELEX: 421792

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; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3480 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-418-848A-4

Query Match 98.8%; Score 127.4; DB 2; Length 3480;

Best Local Similarity 99.2%; Pred. No. 1.4e-32;

Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1981 TTATTCATAATGATAGTAGGAGGCTTCGTAGGTTTAAAGAAATAGTTTTTGTGCTACTTTCT 2040

QY 61 GTAGTGAATAGAGTTAGGCGAGGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 120

Db 2041 ATAGTGAATAGAGTTAGGCGAGGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 2100

QY 121 CCGAGGGGA 129

Db 2101 CCGAGGGGA 2109

RESULT 15

US-08-418-848A-5

; Sequence 5, Application US/08418848A

; Patent No. 5847096

; GENERAL INFORMATION:

; APPLICANT: SCHUBERT, MANFRED, HARMISON II,

; APPLICANT: GEORGE G., CHANG-JIE, CHEN, BANJERJEA, AKHIL

; TITLE OF INVENTION: DEFECTIVE, INTERFERING

; TITLE OF INVENTION: HIV PARTICLES

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; COUNTRY: U.S.A.

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/418,848A

; FILING DATE: 07-APR-1995

; CLASSIFICATION: 526

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/936,849

; FILING DATE: 28-AUG-1992

; CLASSIFICATION: 526

; ATTORNEY/AGENT INFORMATION:

; NAME: RICHARD W. BORK

; REGISTRATION NUMBER: 36,459

; REFERENCE/DOCKET NUMBER: 2026-4091US2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-758-4800

; TELEFAX: 212-751-6849

; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3721 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-418-848A-5

Query Match

Best Local Similarity 98.8%; Score 127.4; DB 2; Length 3721;

Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:52:43 ; Search time 806.349 Seconds
(without alignments)
6934.037 Million cell updates/sec

Title: US-10-003-035-75

Perfect score: 129

Sequence: 1 ttattcataatgatagtagg.....acctccaatcccgagg93ga 129

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
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- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
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- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rtd.*
- 36: em.htg.rtd.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	129	100.0	861	6	I02160	I02160 Sequence 1
2	129	100.0	1026	6	I02162	I02162 Sequence 3
3	129	100.0	2237	6	E02028	E02028 DNA sequence
4	129	100.0	2552	6	I05789	I05789 Sequence 8
5	129	100.0	2945	6	AR365081	AR365081 Sequence
6	129	100.0	3156	6	E01088	E01088 Nucleic aci
7	129	100.0	3156	14	HIVXK3	M14100 Human immun
8	129	100.0	8932	14	HIVH102	M15654 Human immun
9	129	100.0	8933	6	AR094659	AR094659 Sequence
10	129	100.0	8933	6	AR382018	AR382018 Sequence
11	129	100.0	8933	6	AX078307	AX078307 Sequence
12	129	100.0	8933	6	AX078308	AX078308 Sequence
13	129	100.0	8933	6	AX078313	AX078313 Sequence
14	129	100.0	9748	6	E01099	E01099 DNA sequenc
15	129	100.0	9748	14	REH1V3	X01762 Human T-cel
16	129	100.0	9749	6	I07983	I07983 Sequence 1
17	129	100.0	9781	14	HIVF12CG	Z11530 Human Immun
18	129	100.0	9918	12	AF430344	AF430344 Synthetic
19	128	99.2	9795	14	HIVTH475A	L31963 Human immun
20	127.4	98.8	2148	6	BD238379	BD238379 Virus vac
21	127.4	98.8	2148	6	AX032757	AX032757 Sequence
22	127.4	98.8	2264	6	I06771	I06771 Sequence 8
23	127.4	98.8	2559	14	AY426102	AY426102 HIV-1 iso
24	127.4	98.8	2559	14	AY426103	AY426103 HIV-1 clo
25	127.4	98.8	2559	14	AY426104	AY426104 HIV-1 iso
26	127.4	98.8	2559	14	AY426105	AY426105 HIV-1 clo
27	127.4	98.8	2559	14	AY426106	AY426106 HIV-1 clo
28	127.4	98.8	2559	14	AY426107	AY426107 HIV-1 clo
29	127.4	98.8	2559	14	AY426108	AY426108 HIV-1 clo
30	127.4	98.8	2559	14	AY426109	AY426109 HIV-1 clo
31	127.4	98.8	2562	6	AX166280	AX166280 Sequence
32	127.4	98.8	2565	6	BD000747	BD000747 Recombembi
33	127.4	98.8	2896	6	AR264703	AR264703 Sequence
34	127.4	98.8	2730	6	AR097865	AR097865 Sequence
35	127.4	98.8	2940	6	AR064430	AR064430 Sequence
36	127.4	98.8	3426	6	AR064429	AR064429 Sequence
37	127.4	98.8	3480	6	AR064431	AR064431 Sequence
38	127.4	98.8	3721	6	AR064432	AR064432 Sequence
39	127.4	98.8	3993	6	AR064433	AR064433 Sequence
40	127.4	98.8	4059	6	AR064434	AR064434 Sequence
41	127.4	98.8	4632	6	AR064435	AR064435 Sequence
42	127.4	98.8	6229	6	BD238380	BD238380 Virus vac
43	127.4	98.8	6229	6	AX032758	AX032758 Sequence
44	127.4	98.8	7399	6	AR064436	AR064436 Sequence
45	127.4	98.8	9000	14	HIV1U26942	U26942 Human immun

ALIGNMENTS

RESULT 1	I02160	I02160	Sequence 1 from Patent US 4861707.	861 bp ss-DNA	linear	PAT 21-MAY-1993
LOCUS	I02160	I02160	Sequence 1 from Patent US 4861707.			
DEFINITION	I02160	I02160	Sequence 1 from Patent US 4861707.			
ACCESSION	I02160	I02160	Sequence 1 from Patent US 4861707.			
VERSION	I02160.1	GI:270316				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 861)					
AUTHORS	Ivanoff,L.A. and Petteway,S.R.					
TITLE	Human immunodeficiency virus antigen					
JOURNAL	Patent: US 4861707-A 1 29-AUG-1989,					
	E. I. Du Pont de Nemours and Company; Wilmington, DE					


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Best Local Similarity 100.0%; Pred. No. 4.2e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTGCTGTACTTTCT 60
Db 655 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTGCTGTACTTTCT 714

Qy 61 GTAGTGAATAGTAGGAGGATATTCACCATTCATCGTTTCAGACCCACCTCCCAATC 120
Db 715 GTAGTGAATAGTAGGAGGATATTCACCATTCATCGTTTCAGACCCACCTCCCAATC 774

Qy 121 CCGAGGGGA 129
Db 775 CCGAGGGGA 783

RESULT 2
I02162      102162      1026 bp ss-DNA      linear      PAT 21-MAY-1993
DEFINITION   Sequence 3 from Patent US 4861707.
ACCESSION   I02162
VERSION      I02162.1 GI:270318
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 1026)
AUTHORS     Ivanoff,L.A. and Petteway,S.R.
TITLE       Human immunodeficiency virus antigen
JOURNAL     Patent: US 4861707-A 3 29-AUG-1989;
            E. I. Du Pont de Nemours and Company; Wilmington, DE

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Best Local Similarity 100.0%; Pred. No. 4.1e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 820 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTGCTGTACTTTCT 879

Qy 61 GTAGTGAATAGTAGGAGGATATTCACCATTCATCGTTTCAGACCCACCTCCCAATC 120
Db 880 GTAGTGAATAGTAGGAGGATATTCACCATTCATCGTTTCAGACCCACCTCCCAATC 939

Qy 121 CCGAGGGGA 129
Db 940 CCGAGGGGA 948

RESULT 3
E02028
LOCUS        E02028      2237 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION   DNA sequence coding for gag-env hybrid protein.
ACCESSION   E02028
VERSION      E02028.1 GI:2170276
KEYWORDS     JP 1989179687-A/1.
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE    1 (bases 1 to 2237)
AUTHORS     Nozaki,C., Matsushita,S., Hattori,T. and Takatsuki,K.
TITLE       HIV FUSED PROTEIN
JOURNAL     Patent: JP 1989179687-A 1 17-JUL-1989;
            CHEMO SERO THERAPEUT RES INST
            PN JP 1989179687-A/1
            PD 17-JUL-1989
            PF 30-DEC-1987 JP 1987336292
            PI NOZAKI CHIKAHIDE, MATSUSHITA SHUZO, HATTORI TOSHIO, PI
            TAKATSUKI KIYOSHI
            PC C12N7/04,C07K13/00,C12P21/02//A61K39/21,C12N15/00,(C12P21/02,
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            PC (C12N15/00,C12R1:91);
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            CC topology: Linear;
            CC hypothetical: No;
            CC anti-sense: No;
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Best Local Similarity 100.0%; Pred. No. 4e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1609 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTGCTGTACTTTCT 1668

Qy 61 GTAGTGAATAGTAGGAGGATATTCACCATTCATCGTTTCAGACCCACCTCCCAATC 120
Db 1669 GTAGTGAATAGTAGGAGGATATTCACCATTCATCGTTTCAGACCCACCTCCCAATC 1728

Qy 121 CCGAGGGGA 129
Db 1729 CCGAGGGGA 1737

RESULT 4
I05789
LOCUS        I05789      2552 bp      DNA      linear      PAT 02-DEC-1994
DEFINITION   Sequence 8 from Patent EP 0272858.
ACCESSION   I05789
VERSION      I05789.1 GI:590911
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 2552)
AUTHORS     Rusche,J., Lynn,D., Carson,H., Putney,S. and Jellis,C.L.
TITLE       Recombinant HIV envelope proteins produced in insect cells
JOURNAL     Patent: EP 0272858-A2 8 29-JUN-1988;
            Location/Qualifiers
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            /mol_type='unassigned DNA'

ORIGIN
Query Match      100.0%; Score 129; DB 6; Length 2552;
Best Local Similarity 100.0%; Pred. No. 4e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTGCTGTACTTTCT 60
Db 2035 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTGCTGTACTTTCT 2094

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QY 61 GTAGTGAATAGAGTTAGGAGGAGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 120
DB 2095 GTAGTGAATAGAGTTAGGAGGAGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 2154
QY 121 CCGAGGGGA 129
DB 2155 CCGAGGGGA 2163

RESULT 5
LOCUS AR365081 2945 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 1 from patent US 5462872.
ACCESSION AR365081
VERSION AR365081.1 GI:34428384
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2945)
AUTHORS Jonak,Z.L., Debouck,C., Clark,R. and Trulli,S.
TITLE Human lymphoid cells expressing human immunodeficiency virus envelope protein GP160
JOURNAL Patent: US 5462872-A 1 31-OCT-1995;
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.9e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2317 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAAATAGTTTTCGTCTACTTTCT 2376

QY 61 GTAGTGAATAGAGTTAGGAGGAGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 120
DB 2377 GTAGTGAATAGAGTTAGGAGGAGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 2436

QY 121 CCGAGGGGA 129
DB 2437 CCGAGGGGA 2445

RESULT 6
LOCUS E01088 3156 bp DNA linear PAT 29-SEP-1997
DEFINITION Nucleic acid sequence coding for HTLV envelop protein.
ACCESSION E01088
VERSION E01088.1 GI:2169347
KEYWORDS JP 1987012799-A/1.
SOURCE unidentified
ORGANISM unclassified

REFERENCE 1 (bases 1 to 3156)
AUTHORS Robaato,M.K., Robaato,C.G., Bragamu,P.R., Jiyooji,M.S. and Furutsushii,I.U.
TITLE ENVELOPE PROTEIN OF VIRUS OF ACQUIRED IMMUNODEFICIENCY SYNDROME
JOURNAL Patent: JP 1987012799-A 1 21-JAN-1987;
F HOFFMANN LA ROCHE & CO AG, USA GOVERNMENT
COMMENT OS Human (Homo sapiens)
PN JP 1987012799-A/1
PD 21-JAN-1987
PF 18-APR-1986 JP 1986089830
PR 19-APR-1985 US 85 725021
PI ROBAATO MITSUHIRO KUROU, ROBAATO CHIYARUZU GARO, PI ERAGAMU FUREMUKUMAA REDEI, JIYOOJI METSUDO SHIYOU, PI FURUTSUSHII ICHINGU UONGUSUTARU
PC C07K13/00,A61K39/21,C07H21/04,C12N1/20,C12N15/00,C12P21/00, PC

CL12P21/02,
PC G01N33/569,G01N33/577,(C12N1/20,C12R1:125),(C12N1/20,C12R1:19),PC (C12P21/02,
PC C12R1:125),(C12P21/02,C12R1:19);
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: library=genome library;
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.9e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GTAGTGAATAGAGTTAGGAGGAGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 120
DB 2587 GTAGTGAATAGAGTTAGGAGGAGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 2646

QY 121 CCGAGGGGA 129
DB 2647 CCGAGGGGA 2655

RESULT 7
LOCUS HIVHXB3 3156 bp ss-RNA linear VRL 02-AUG-1993
DEFINITION Human immunodeficiency virus type 1, isolate HXB3, env region.
ACCESSION M14100
VERSION M14100.1 GI:327751
KEYWORDS Human immunodeficiency virus 1 (HIV-1)
SOURCE Human immunodeficiency virus 1
ORGANISM Viruses; Retroviridae; Retroviridae; Lentivirus; Primate
REFERENCE 1 (bases 1 to 3156)
AUTHORS Crowl,R., Ganguly,K., Gordon,M., Conroy,R., Schaber,M., Kramer,R., Shaw,G., Wong-Staal,F. and Reddy,E.P.
TITLE HTLV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients
JOURNAL Cell 41 (3), 979-986 (1985)
MEDLINE 85228248
COMMENT PUBMED 2988795
Original source text: Human immunodeficiency virus type 1 (HIV-1), isolate HXB3, proviral DNA.

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/translation="MGGKWSKSSVVGWPAVRMRMRAPPAADGVGAASR"
/translation approx. 88 bp upstream of tat initiation codon.

ORIGIN      EcoRI site approx. 88 bp upstream of tat initiation codon.
Query Match      100.0%; Score 129; DB 14; Length 3156;
Best Local Similarity 100.0%; Pred. No. 3.9e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTATTCATATCATAGTAGGAGCTTGGTAGTTTAAAGATAGTTTTTGGCTGTACTTTCT 60
DB      2527 TTATTCATATCATAGTAGGAGCTTGGTAGTTTAAAGATAGTTTTTGGCTGTACTTTCT 2586
QY      61 GTAGTGAATAGTAGTAGGAGGATATTCACCATTCATCGTTTCAGACCCCACTCCCAATC 120

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Db 2587 GTAGTGAATAGTAGGAGGATATTCACCATTCATCGTTTCAGACCCCACTCCCAATC 2646

QY 121 CCGAGGGGA 129

Db 2647 CCGAGGGGA 2655

RESULT 8

HIVBH102

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

8932 bp ss-RNA linear VRL 02-AUG-1993

Human immunodeficiency virus type 1, isolate BH10, genome.

M15654 K02008 K02009 K02010

VERSION

M15654.1 GI:32683

TAR region: acquired immune deficiency syndrome; env protein; gag protein; long terminal repeat (LTR); pol protein; polyprotein; proviral gene; reverse transcriptase; transactivator.

2 of 2

SEGMENT

SOURCE

ORGANISM

Human immunodeficiency virus 1 (HIV-1)

Viruses; Retrovirdae; Retroviridae; Lentivirus; Primate lentivirus group.

1 (bases 1 to 8932)

Wong-Staal,F., Gallo,R.C., Chang,N.T., Grayeb,J., Papas,T.S., Lautenberger,J.A., Pearson,M.L., Petteway,S.R.Jr., Ivanoff,L., Baumeister,K., Whitehorn,E.A., Rafalski,J.A., Doran,E.R., Josephs,S.J., Starcich,B., Livak,K.J., Patarca,R., Haseltine,W.A. and Ratner,L.

Complete nucleotide sequence of the AIDS virus, HTLV-III

Nature 313 (6000), 277-284 (1985)

85111123

PUBMED

2578615

REFERENCE

2 (bases 1 to 8932)

van Beveren,C.P., Coffin,J. and Hughes,S.

Appendix B: HIV-3 genome

(in) Weiss,R.L., Teich,N., Varmus,H. and Coffin,J. (Eds.);

RNA TUMOR VIRUSES, MOLECULAR BIOLOGY OF TUMOR VIRUSES, SECOND EDITION, 2;

Cold Spring Harbor Laboratory, CSH, NY (1985)

3 (sites)

Hostonsky,Z., Hostonska,Z., Hudson,G.O., Moonaw,E.W. and Nides,B.R.

Reconstitution in vitro of RNase H activity by using purified N-terminal and C-terminal domains of human immunodeficiency virus type 1 reverse transcriptase

Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1148-1152 (1991)

91142129

MEDLINE

1705027

COMMENT

Original source text: Human immunodeficiency virus type 1 (HIV-1) proviral DNA clone BH10.

[(in) Weiss,R., Teich,N., Varmus,H. and Coffin,J. (Eds.); RNA Tumor Viruses,Molecu] review; bases 1 to 8932.

The BH10 sequence differs from BH8 and BH5 by 0.9% in the coding regions and 1.8% in the noncoding regions, and the authors of [1] believe that these are stable variants.

The HTLV-III genome encodes at least seven proteins: gag, pol, env, tat, trs, 27K antigen and the sor 23K product. The 3' ORF (positions 8153-8773) is truncated in BH10 (stop codon at positions 8522-8524), but reads through in BH8 and other sequences to yield what is now called the 27K antigen.

The mechanism for pol gene translation has not been elucidated: a gag-pol fusion protein is possible; splicing or frameshift have not been ruled out. The viral protease would be determined by the region in question.

The tat protein (trans-activator protein, approximately 14 kb) is an effector of an autostimulatory pathway through interaction with a positive control element, the trans-activating responsive sequence, TAR. Tat seems to be a transcriptional control molecule in HTLV-1, but is both that and a post-transcriptional regulatory molecule in HTLV-III. Deletion mutants in the tat gene are incapable of prolific replication and exhibit no cytopathic effects in T4 cell lines.

In addition to the

9.4 kb genomic mRNA, subgenomic mRNAs of 7.4, 5.5, 5.0, 4.3, 2.0

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and 1.8 kb have been detected.
FEATURES             Location/Qualifiers
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                        /mol_type="genomic RNA"
                        /db_xref="taxon:11676"
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                        /note="genomic mRNA"
     prim_transcript   <1..>8932
                        /note="tat, rev, nef subgenomic mRNA"
     intron            66..5135
                        /note="tat, rev, nef subgenomic mRNA intron 1"
                        112..11650
     CDS               /note="gag polyprotein precursor"
                        /codon_start=1
                        /protein_id="AAA44201.1"
                        /db_xref="GI:326388"
                        /translation="MGARASVLSGGELDRWEKIRLRPGKKYKYLKHIVWASRELERP
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KIBEEQNKSKKQAQAADTGHSSQVSNPTIVQNIQOMVHOAISPTLNAMVYVE
EXAFSPVIMFSAISGATPDINTMLNTVGGHQAOMLKETINEEAEMWVRVHV
HAGPIAQWREPRGSDIAGTSTLQEQIGWMTNPPIPVGEIYKRWIILGNKIVRM
YSPSLIDIQGKEPRDVIDRFYKLRARQASQEVKNWMTETLLWONAPDCKTIL
KALGPAALTEEMTACQGVGPGHKARVLAAWSQVTNTATIMQRFNFRQRMVKC
FNCQKEGHTARNCRAPKKGCKGCKEGHQMDCTERQANFLGKIWPSYKGRPNFLQ
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                        /gene="pol"
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                        /gene="pol"
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                        /codon_start=1
                        /product="pol polyprotein"
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                        /db_xref="GI:326385"
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WGRDNNSPSEAGADRGCTVSFNPQITLWQRPVITIKIGQKLEALLDTCADDTVLE
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IGCTLNPISPIETVPKLAGMDGPKVQWPLTEEKIKALVELICTEMEGKLSKIG
PENPYNTVPAIKKDSKTWRKLVDFRELNRKTQDFWEVQGLGPHPLAGLKKKSVTVL
DVGDAVPSLDEDFRYTAPTIPSINNETPGIQNVNLPQMGKSPALFQSSMTKI
LEPPKQDPDVTQVQVPIVPSGDLGIGQRTKIEELRQLRWGLTTPDKHQKEP
PFLWNGYELPDKWTQVPIVPEKDSWTVNDIOKLVGKLNWASOIVPGIKVOLCKLL
RGTKALTEVPLTEAELEAENREILKEPVHGVYDPSKDLAIIQKQOGQGVTOI
YQPEFKNLTKGYABMGANDNVKQLTEAVQKLTIESIVIWGKTPEKPLIQKETEWE
TWTEYQWATWIPWEFVNTPLVLKMLEKEPIVGAETPIVDGAANRTKLGKAGT
VTNKGQKVPNTNTNQKTELQALYLALQDSGLEVINIVTDSQALGIIQAPDKSES
ELVNQIIIEQLIKKEVYLAWPAHKGIGGNEQVDKLSAGIRKILFDGDKAQDEHE
KYHSNMRAMASDFNLPPVAKIEIVASCDKQLKGBAMHGOVDCSPGIWQDCDTHLEK
VILVAVHVSQYIEAEVIPAETGOETAYFLIKLAGRPVKTITHDWSNFTSATVAA
CWAGIKQEFGIYPNQSQGVESMKNELKKIIGQVRDQAEHLKTAQVMAVFTHNFKR
KGGIGGYASGERIVDIIATDIOTKELQKITKIONFVYVDYDNRNPLWKGPALLWKG
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                        /protein_id="AAA44202.1"
                        /db_xref="GI:326389"
                        /translation="MENRWQVIMVQVDRMRIRTWKSLVHKHMVUSKARGWYRHHY
ESPHRISSEVHIPGLDARLIVITVGLHTGERDWHIGQGVSEIWRKKRYSTQVDPPEL
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PPLPSVTKLTEDRWNKPKQTKGHRGSHTMNGH"
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/db_xref="GI:326386"
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/protein_id="AAA44200.1"
/db_xref="GI:326387"
/translation="MAGRSGSDSDLLKAVRLIKFLYQSNPPNPPECTROARRRRR
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LVESPTVLSGAKE"
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5420..5665
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5580..8150
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QHEDTIISLDQSLKPCVKLTPLCVSLKCTDLKNDTNTSSSGRMIMKEGEIKNCSEF
ISISIRGKYQKVEAFYKLDLIPIDNDTSYTLTSCNTSVITQACPKVSEPIPIHC
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FTDNAKTIIQLNQSVINCTRENNTKRSIRIQRGPRAFVTIKIGNNRQHCNIS
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GLLITRDGNSNNESIIPFGCGMDMRSELYKYVKVLEPLGVAPTKAKRVVQR
EKRAVIGALFLGLAAGSTMGASMTLVQARQLLSGLVQOQNLLRALEAQHLL
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NMWMEWDEINNTSLIHSLEESQOQEKNSOELLELDKWSLWNNFNTIWMYI
KLFIMTVGGLVGLIRIVFVLSVNVVRQGYSPLSFQTHLPPIPRGPRPEGIEEGGER
DRDRSIRLVGSLALWDDLRLSLCLFSYHRLDLLLITVRIVELLGRGWALKYWN
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7734..>8008
/note="rev protein"
/number=3
7734..>7779
/note="tat protein"
/number=3
8152..8523
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Qy      1  TTATTCAATGATAGTAGGAGCGCTGGTAGGTTAAGATAGTCTTTTGTGCTACTTTCT 60
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Db      7629 TTATTCAATGATAGTAGGAGCGCTGGTAGGTTAAGATAGTCTTTTGTGCTACTTTCT 7688

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QY 61 GTAGTGAATAGAGTTAGGAGGGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 120
|||||
Db 7689 GTAGTGAATAGAGTTAGGAGGGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 7749

QY 121 CCGAGGGGA 129
|||||
Db 7749 CCGAGGGGA 7757

RESULT 9
AR094659 AR094659 8933 bp DNA linear PAT 08-SEP-2000
LOCUS
DEFINITION Sequence 4 from patent US 6001977.
ACCESSION AR094659
VERSION AR094659.1 GI:10021783
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 8933)
AUTHORS Chang,N.T., Gallo,R.C. and Wong-Staal,F.
TITLE Cloning and expression of HTLV-III DNA
JOURNAL Patent: US 6001977-A 4 14-DEC-1999;
FEATURES
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ORIGIN
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Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 7630 TTATTCATAATGATAGTAGGAGGCTTGTTAGGTTTAAAGATAGTTTTTGGCTGTACTTTCT 7689

QY 61 GTAGTGAATAGAGTTAGGAGGGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 120
|||||
Db 7690 GTAGTGAATAGAGTTAGGAGGGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 7749

QY 121 CCGAGGGGA 129
|||||
Db 7750 CCGAGGGGA 7758

RESULT 10
AR382018 AR382018 8933 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 4 from patent US 6610476.
ACCESSION AR382018
VERSION AR382018.1 GI:40090419
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 8933)
AUTHORS Chang,N.T., Gallo,R.C. and Wong-Staal,F.
TITLE Detection of HIV-1 DNA
JOURNAL Patent: US 6610476-A 4 26-AUG-2003;
FEATURES
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1. .8933
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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|||||
Db 7690 GTAGTGAATAGAGTTAGGAGGGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 7749

QY 121 CCGAGGGGA 129
|||||
Db 7750 CCGAGGGGA 7758

RESULT 11
AX078307 AX078307 8933 bp RNA linear PAT 22-FEB-2001
LOCUS
DEFINITION Sequence 3 from Patent WO0107661.
ACCESSION AX078307
VERSION AX078307.1 GI:13157998
KEYWORDS
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
REFERENCE 1
AUTHORS Nunomura,K.
TITLE Polynucleotide amplification method
JOURNAL Patent: WO 0107661-A 3 01-FEB-2001;
FEATURES
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/organism="Human immunodeficiency virus"
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/note="Sequence of transcripts produced from the BH10 plasmid."

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.7e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 7630 TTATTCATAATGATAGTAGGAGGCTTGTTAGGTTTAAAGATAGTTTTTGGCTGTACTTTCT 7689

QY 61 GTAGTGAATAGAGTTAGGAGGGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 120
|||||
Db 7690 GTAGTGAATAGAGTTAGGAGGGATATTCACCATTTATCGTTTCAGACCCACCTCCCAATC 7749

QY 121 CCGAGGGGA 129
|||||
Db 7750 CCGAGGGGA 7758

RESULT 12
AX078308 AX078308 8933 bp RNA linear PAT 22-FEB-2001
LOCUS
DEFINITION Sequence 4 from Patent WO0107661.
ACCESSION AX078308
VERSION AX078308.1 GI:13157999
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Nunomura,K.
TITLE Polynucleotide amplification method
JOURNAL Patent: WO 0107661-A 4 01-FEB-2001;
FEATURES
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1. .8933
/organism="synthetic construct"
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/note="Sequence of the IAC-Asrc pseudo target"
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variation
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/Note="Mutated positions: 4135, 4140-1, 4145, 4150,
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.7e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGATAGTTTTCGTGCTACTTCT 60
Db 7630 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGATAGTTTTCGTGCTACTTCT 7689

QY 61 GTAGTGAATAGTAGGAGGATATTCACCATTCGTTTCAGACCCACCTCCCAATC 120
Db 7690 GTAGTGAATAGTAGGAGGATATTCACCATTCGTTTCAGACCCACCTCCCAATC 7749

QY 121 CCGAGGGGA 129
Db 7750 CCGAGGGGA 7758

RESULT 13
AX078313
LOCUS AX078313 8933 bp RNA linear PAT 22-FEB-2001
DEFINITION Sequence 9 from Patent WO0107661.
ACCESSION AX078313
VERSION AX078313.1 GI:13158004
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Nunomura,K.
TITLE Polynucleotide amplification method
JOURNAL Patent: WO 0107661-A 9 01-FEB-2001;
Gen-Probe Incorporated (US)
FEATURES
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/db_xref="taxon:32830"
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variation
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.7e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGATAGTTTTCGTGCTACTTCT 60
Db 7630 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGATAGTTTTCGTGCTACTTCT 7689

QY 61 GTAGTGAATAGTAGGAGGATATTCACCATTCGTTTCAGACCCACCTCCCAATC 120
Db 7690 GTAGTGAATAGTAGGAGGATATTCACCATTCGTTTCAGACCCACCTCCCAATC 7749

QY 121 CCGAGGGGA 129
Db 7750 CCGAGGGGA 7758

RESULT 14
E01099
LOCUS E01099 9748 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence coding for HTLV-III polypeptide.
ACCESSION E01099
VERSION E01099.1 GI:2169358
KEYWORDS JP 1987026300-A/1
SOURCE Homo sapiens (human)

```

```

ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9748)
AUTHORS Nanshi,T.C.
TITLE CLONING AND DEVELOPING OF HTLV-III DNA
JOURNAL Patent: JP 1987026300-A 1 04-FEB-1987;
SENTOKO INC
COMMENT OS human(homo sapiens)
PN JP 1987026300-A/1
PD 04-FEB-1987
PF 11-OCT-1985 JP 1985226658
PR 10-OCT-1984 US 84 659339, 23-JAN-1985 US 85 693866 PI
NANSHI TEI CHIAN
PC C07K13/00,A61K39/21,A61K39/395,C07H21/04,C07K15/12,C12N5/00,
C12N15/00,
PC C12P21/00,C12Q1/68,G01N33/574,G01N33/577;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
FH Key
FH 5'UTR 1..786
FT promoter 579..786
FT mat_peptide 787..1182
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FT mat_peptide 1182..1185
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Best Local Similarity 100.0%; Pred. No. 3.7e-28;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GTAGTGAATAGTAGGAGGATATTCACCATTCGTTTCAGACCCACCTCCCAATC 120
Db 8363 GTAGTGAATAGTAGGAGGATATTCACCATTCGTTTCAGACCCACCTCCCAATC 8422

QY 121 CCGAGGGGA 129
Db 8423 CCGAGGGGA 8431

RESULT 15
REHTLV3
LOCUS REHTLV3 9748 bp RNA linear VRL 12-JUL-1999
DEFINITION Human T-cell leukaemia type III (HTLV-III) proviral genome (AIDS virus for acquired immune deficiency syndrome).

```

Search completed: March 11, 2004, 21:24:09
Job time : 808.349 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 19:37:35 ; Search time 1731.47 Seconds
(without alignments)
1552.207 Million cell updates/sec

Title: US-10-003-035-74
Perfect score: 90
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
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8: em_esti:*
9: gb_esti:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
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27: em_gss_vri:*
28: gb_gsa1:*
29: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	88.4	98.2	527	28	BH886550
C 3	34	37.8	809	29	CG887892
C 4	34	37.8	925	29	CC714059

5	32.6	36.2	473	14	CD850313
6	32	35.6	454	14	CD230371
7	32	35.6	515	14	CD220247
8	31	34.4	940	29	CG172989
9	30.6	34.0	634	14	CA485128
10	30.2	33.6	225	9	AA879214
11	30.2	33.6	274	9	AA879214
12	30.2	33.6	294	9	AA932668
13	30.2	33.6	301	12	EG986731
14	30.2	33.6	386	10	AW788422
15	30.2	33.6	400	10	AW788422
16	30.2	33.6	419	9	AI191724
17	30.2	33.6	453	14	CB242078
18	30.2	33.6	703	14	CB240983
19	30.2	33.6	897	13	BU508236
20	30.2	33.6	971	13	CA160629
21	30	33.3	598	29	CG411974
22	30	33.3	1124	12	BM906828
23	29.8	33.1	512	9	AL925118
24	29.6	32.9	524	28	AZ245786
25	29.6	32.9	545	29	DR21G95
26	29.6	32.9	568	12	BM303578
27	29.6	32.9	680	28	AZ285851
28	29.4	32.7	601	10	AW763087
29	29.4	32.7	681	10	BF035293
30	29	32.2	381	13	C69365
31	29	32.2	538	13	BM200729
32	29	32.2	634	29	AG175005
33	29	32.2	1221	28	CC315338
34	28.8	32.0	247	10	BF910948
35	28.8	32.0	521	10	BB283870
36	28.8	32.0	688	28	BZ434193
37	28.8	32.0	774	10	BF182322
38	28.8	32.0	838	28	BH529684
39	28.8	32.0	940	29	CG060838
40	28.8	32.0	958	28	CC285079
41	28.8	32.0	1014	28	BZ474051
42	28.8	32.0	1064	28	CC285081
43	28.6	31.8	222	9	AA872865
44	28.6	31.8	257	9	AA865648
45	28.6	31.8	330	9	AI916409

ALIGNMENTS

RESULT 1
AB036462/c
LOCUS
DEFINITION
AB036462 Mus musculus Cj7 brain, liver, kidney, lung, heart, spleen
Mus musculus CDNA clone 13-3, mRNA sequence.
317 bp mRNA linear EST 22-AUG-2000
ACCESSION
AB036462
VERSION
AB036462.1 GI:6854195
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 317)
Wang, Y.L., Saigoh, K., Osaka, H., Yamaniishi, T., Kiyosawa, H., Sakai, Y., Wakana, S. and Wada, K.
YAC/BAC-Based physical and transcript mapping around the gracile axonal dystrophy (gad) locus identifies uchli, pmx2b, atp3a2, and hip2 genes
Genomics 66 (3), 333-336 (2000)

CONTACT: Keiji Wada
Department of Degenerative Neurological Diseases
National Institute of Neuroscience, NCNP
4-1-1, Ogawahigashi, Kodaira, Tokyo 187-8502, Japan
Email: wada@ncnp.go.jp
RT-PCR primer based on the sequence that isolated from mouse BAC

clones (437N8, 538024, Research Genetics) using exon trapping method.

FEATURES

source
1. 317
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129/Sv"
/db_xref="taxon:10090"
/map="5"
/clones="13-3"
/sex="male"
/tissue_type="brain,liver,kidney,lung,heart,spleen"
/cell_line="C17 embryonic stem cell line"
/dev_stage="adult"
/clone_lib="Mus musculus C17 brain, liver, kidney, lung, heart, spleen"

ORIGIN

Query Match 100.0%; Score 90; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 60
Db |||||
141 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 82
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 81 CTCCTTGGGATGTTGATGATCTGTAGTGCT 52

RESULT 2

BH886550/c
LOCUS
DEFINITION BH886550.1 Leishmania major Friedlin BAC Library Leishmania major genomic clone LB00861a, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 527)
Myler,P.J., Vogt,C., Munden,H., Robertson,L., Sisk,E.,
Fazelinia,G., Aggarwal,G., Nelson,S., Seyler,A., Worthey,E.,
Stuart,K. and Ragland,M.
Leishmania major Friedlin BAC End Sequences
Unpublished (2002)
Other_GSSs: LB00861a.d.T7.1
Contact: Myler PJ
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-0313
Email: mylerpj@sbri.org
Seq primer: Sp6
Class: BAC ends.

FEATURES

source
1. 527
/organism="Leishmania major"
/mol_type="genomic DNA"
/strain="Friedlin"
/db_xref="taxon:5664"
/clones="LB00861a"
/lab_host="E. coli GeneHogs + Trfa"
/clone_lib="Leishmania major Friedlin BAC Library"
/note="Vector: pCG270; Site 1: HindIII; Genomic DNA from Leishmania major Friedlin in agarose blocks was partially digested with HindIII, size selected, and ligated with HindIII-digested pCG270 vector DNA. 10368 clones were picked and arrayed in 384- and 96-well plates. Library construction and arraying was carried out by ResGen Corporation and clones and filters are available from

ORIGIN

Query Match 98.2%; Score 88.4; DB 28; Length 527;
Best Local Similarity 98.9%; Pred. No. 4.7e-14;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 60
Db |||||
266 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 207
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
Db 206 CTCCTTGGGATGTTGATGATCTGTAGTGCT 177

RESULT 3

CG687892
LOCUS
DEFINITION ZMMBBC0165L22r ZMMBBC (EcoRI) Zea mays subsp. mays genomic clone ZMMBBC0165L22 3', genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 809)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Ming,R. and Messing,J.
Sequencing of the maize genome at PGIR (2003c)
Unpublished (2003)
Contact: Bharti,A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 400.

FEATURES
source
1. 809
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBBC0165L22"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBC (EcoRI)"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI"

ORIGIN

Query Match 37.8%; Score 34; DB 29; Length 809;
Best Local Similarity 63.4%; Pred. No. 50;
Matches 52; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 2 TGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 61
Db |||||
575 TGAGTCTGCATGAGAAACATCTGCATATGTCATTGGAGGTGGTGGAGGCACTGC 634
QY 62 TCCTTGGGATGTTGATGATCTG 83
Db 635 TGCTGGGGTGGCTCATCATGTG 656

RESULT 4

CC714059

LOCUS
 DEFINITION CC714059 925 bp DNA linear GSS 19-JUN-2003
 OGUBX71TV ZM 0.7 1.5_KB Zea mays genomic clone ZMMBMA0404K22,
 genomic survey sequence.
 ACCESSION CC714059
 VERSION CC714059.1 GI:32118835
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 925)
 White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)
 COMMENT Other_GSSs: OGUBX71TH
 Contact: Cathy Whitelaw
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TP
 Class: sheared ends.
 Location/Qualifiers
 1..925
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBMA0404K22"
 /clone_lib="ZM 0.7 1.5_KB"
 /note="Vector: pBOSK-; Site 1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"

ORIGIN
 Query Match 37.8%; Score 34; DB 29; Length 925;
 Best Local Similarity 63.4%; Pred. No. 53;
 Matches 52; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 QY 2 TGAGAGTGAAGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATGC 61
 DB 342 TGAGTCTGATGAGAAACATCTCTATTGATTCATTCGGGGTGGTGGAGGAGCAATGC 401
 QY 62 TCCTGGGATGTGATGATCTG 83
 DB 402 TGCTGGGGTCCATCATGTG 423

RESULT 5
 LOCUS CD850313 473 bp mRNA linear EST 11-JUL-2003
 DEFINITION DH0AC382A11RM1 HaDevR2 Helianthus annuus cDNA clone HaDevR238A11,
 mRNA sequence.
 ACCESSION CD850313
 VERSION CD850313.1 GI:32534135
 KEYWORDS EST.
 SOURCE Helianthus annuus (common sunflower)
 ORGANISM Helianthus annuus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulide; Asterales; Asteraceae; Asteroidae;
 Heliantheae; Helianthus.
 1 (bases 1 to 473)
 Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00

LOCUS
 DEFINITION CC714059 925 bp DNA linear GSS 19-JUN-2003
 OGUBX71TV ZM 0.7 1.5_KB Zea mays genomic clone ZMMBMA0404K22,
 genomic survey sequence.
 ACCESSION CC714059
 VERSION CC714059.1 GI:32118835
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 925)
 White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)
 COMMENT Other_GSSs: OGUBX71TH
 Contact: Cathy Whitelaw
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TP
 Class: sheared ends.
 Location/Qualifiers
 1..925
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBMA0404K22"
 /clone_lib="ZM 0.7 1.5_KB"
 /note="Vector: pBOSK-; Site 1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"

ORIGIN
 Query Match 37.8%; Score 34; DB 29; Length 925;
 Best Local Similarity 63.4%; Pred. No. 53;
 Matches 52; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 QY 2 TGAGAGTGAAGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATGC 61
 DB 342 TGAGTCTGATGAGAAACATCTCTATTGATTCATTCGGGGTGGTGGAGGAGCAATGC 401
 QY 62 TCCTGGGATGTGATGATCTG 83
 DB 402 TGCTGGGGTCCATCATGTG 423

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

RESULT 6
 LOCUS CD230371/c 454 bp mRNA linear EST 21-MAY-2003
 DEFINITION SS1_43 D04.b1 A012 Salt-stressed seedlings Sorghum bicolor cDNA
 clone SS1_43_D04_A012 3', mRNA sequence.
 ACCESSION CD230371
 VERSION CD230371.1 GI:30973805
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 454)
 Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S.,
 Klein, R.R., Liang, C., Sun, P., Sullivan, R., Shah, M., Summer, E.J.,
 Eastman, A. and Pratt, L.H.
 An EST database from Sorghum: salt-stressed seedlings
 Unpublished (2003)
 Other_ESTs: SS1_43_D04.g1_A012
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science; plant material and RNA prepared at Texas A & M University;
 sequencing done in the Laboratory for Genomics and Bioinformatics,
 University of Georgia. Sequence ends have been trimmed to exclude
 vector and regions below phred quality 16. Three-prime sequences
 are presented as their reverse complement and have been trimmed to
 exclude polyA.
 Seg primer: Sug3 (CGACCTGCGCTCGAGCACA)
 POLYA=yes.
 Location/Qualifiers
 1..454
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="IS3620C"
 /db_xref="taxon:4558"
 /clone="SS1_43_D04_A012"
 /lab_host="DH10B-T1 phage-resistant E. coli"

FEATURES
 source
 Location/Qualifiers
 1..454
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="IS3620C"
 /db_xref="taxon:4558"
 /clone="SS1_43_D04_A012"
 /lab_host="DH10B-T1 phage-resistant E. coli"

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
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 Location/Qualifiers
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 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
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 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
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 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
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 /db_xref="taxon:4232"
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 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
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 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
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 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="psc8"
 /db_xref="taxon:4232"
 /clone="HaDevR238A11"
 /tissue type="terminal bud"
 /clone_lib="HaDevR2"

ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
 DB 291 AGGACATGGACCACTACTAGCAAACTTGCAGATGAGGGAGGAGGAGGAGAACAG 350
 QY 61 CTCCTGGGATGTTCATGATCTGTAGT 87
 DB 351 CTGCTGCTGGTGAAACCATGTGTAGT 377

FEATURES
 source
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus

/clone lib="salt-stressed seedlings"
 /note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from 9-day-old seedlings grown in hydroponic culture. Seedlings were transferred to a 150 mM NaCl solution and harvested at 3, 6, 12 and 24 hr following transfer. Roots and leaves were pooled from all time points and RNA isolated. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG)."

ORIGIN
 Query Match 35.6%; Score 32; DB 14; Length 454;
 Best Local Similarity 68.8%; Pred. No. 1.4e+02;
 Matches 44; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 23 AGCAGTTGTGAGATGGGGTGGAGATGGGGCACCACATCTCTTGGGATGTTGATGATCT 82
 |||
 Db 97 AGAGTTTGTGAGATGCTGTGTGGAGATTTTGCATGGGGGCGCATTTGGATGTAGATGTTT 38
 |||
 QY 83 GTAG 86
 |||
 Db 37 CGAG 34

RESULT 7
 CD220247/c
 LOCUS
 DEFINITION CC1_66_C06.bl.A007 Callus culture/cell suspension Sorghum bicolor
 CDNA clone CC1_66_C06_A007 3', mRNA sequence.

ACCESSION
 VERSION CD220247.1 GI:30963681
 KEYWORDS
 SOURCE EST
 ORGANISM Sorghum bicolor (sorghum)

REFERENCE
 AUTHORS
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 515)

TITLE
 JOURNAL
 COMMENT
 Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Rathore, K., Eastman, A., and Pratt, L.H.
 An EST database from Sorghum: callus culture and cell suspension Unpublished (2003)
 Other ESTs: CC1_66_C06.g1.A007
 Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: Sug3 (CGACCTGCAGTCGAGCACA)
 POLYA=No.

FEATURES
 source
 Location/Qualifiers
 1..515
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultiivar="RTx430"
 /db_xref="taxon:4558"
 /clone="CC1_66_C06_A007"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_lib="Callus culture/cell suspension"
 /note="Vector: pME18S-FL3; Site_1: XhoI; Site_2: XhoI; The

library was prepared from a mixture of polyA+ RNA from callus cultured tissue and cells in suspension culture. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN
 Query Match 35.6%; Score 32; DB 14; Length 515;
 Best Local Similarity 68.8%; Pred. No. 1.5e+02;
 Matches 44; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 23 AGCAGTTGTGAGATGGGGTGGAGATGGGGCACCACATCTCTTGGGATGTTGATGATCT 82
 |||
 Db 160 AGAGTTTGTGAGATGCTGTGTGGAGATTTTGCAGGGGGCGCATTTGGATGTAGATGTTT 101
 |||
 QY 83 GTAG 86
 |||
 Db 100 GGAG 97

RESULT 8
 CG172989
 LOCUS
 DEFINITION PUPFC46TD ZM 0.6 1.0 KB Zea mays genomic clone ZM8Bta0701G19,
 genomic survey sequence.

ACCESSION
 VERSION CG172989.1 GI:34063787
 KEYWORDS
 SOURCE GSS.

ORGANISM
 Zea mays
 Zea mays

REFERENCE
 AUTHORS
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

TITLE
 JOURNAL
 COMMENT
 Whitelaw, C.A., Fraser, C.M., Yuan, Y., Van Aken, S., Utterback, T., Resnick, A., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
 Maize Genomics Consortium
 Unpublished (2003)
 Other_GSSs: PUPFC46TB
 Contact: Cathy Whitelaw

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5943
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TP
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
 1..940
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZM8Bta0701G19"
 /clone_lib="ZM 0.6 1.0 KB"
 /note="Vector: PCR-T0FO; Site 1: EcoRI; 0.6-1.0 kb high
 Cot selected genomic DNA library"

ORIGIN
 Query Match 34.4%; Score 31; DB 29; Length 940;
 Best Local Similarity 62.0%; Pred. No. 3.6e+02;
 Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 8 TGAGGAGAAATATCAGCATCTGTGGAGATGGGGTGGAGATGGGGCACCACATGCTCTTGG 67
 |||
 Db 146 TGATCCATAAGTTCTCTGCTTGTGGAGTGGGGAGGTGGTGGGGACCTGCTGTTT 205
 |||

QY 68 GGATGTTGATGATCTGTAG 86
 |||
 Db 206 TGCCCGTGACGAGGTCTAG 224

```

RESULT 9
CA485128/c
LOCUS
DEFINITION
WHE4314_G11_M22S Wheat meiotic anther cDNA library Triticum
aestivum CDNA clone WHE4314_G11_M22, mRNA sequence.
ACCESSION
CA485128
VERSION
CA485128.1 GI:24979133
KEYWORDS
EST.
ORGANISM
Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 634)
Anderson, O.D., Chao, S., Crossman, C., Langridge, P., Lazo, G.R.,
Pham, J., Raush, C.J., Sutton, T., Woo, J. and Wilson, C.
The structure and function of the expressed portion of the wheat
genomes - Meiotic anther cDNA library
Unpublished (2002)
JOURNAL
COMMENT
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105959773
Fax: 5105959518
Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer
FEATURES
source
1..634
Location/Qualifiers
/mol_type="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE4314_G11_M22"
/tissue_type="Anther"
/dev_stage="Meiotic stages pre-meiosis-metaphase I"
/lab_host="E. coli DH10B"
/clone_lib="Wheat meiotic anther cDNA library"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Plants
were grown in a glasshouse. Anther meiotic stage was
determined by removing anthers from individual primary
florets. One anther was sacrificed for microscopic
staging, and if determined to be between (and including)
meiotic stages pre-meiosis and metaphase I, the remaining
two anthers were collected and pooled for library
construction. The tissue, total RNA, and poly(A) RNA were
prepared, cDNA synthesised, and directionally ligated into
pSPORT1 by Tim Sutton in the P Langridge Lab at the
Department of Plant Science, University of Adelaide, Waite
Campus, Australia. Average insert size 1.5kb. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
ORIGIN
Query Match 34.0%; Score 30.6; DB 14; Length 634;
Best Local Similarity 60.0%; Pred. No. 3.9e+02;
Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

1 ATGAGAGTGAAGGAGGAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGCACCATG 60
|||||
209 ATGGAAGAAGAGAGGAAGAACCCAGCAAGTAGAGAGGCCAGCCAGCAGTGGATGCACG 150
|||||
61 CTCCTTGGGATGTTGATGTCGTA 85
|||||
149 GTCCTTGGGATGATGAAGAGGGTA 125
|||||

RESULT 10
AA879214/c
LOCUS
DEFINITION
nw85d06.s1 NCI CGAP Pr12 Homo sapiens cDNA clone IMAGE:1253387
similar to contains element MER28 repetitive element ;, mRNA
sequence.
AA879214
VERSION
AA879214.1 GI:2988179
KEYWORDS
EST.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 225)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: sgabres@email.nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.,
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
FEATURES
source
1..225
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1253387"
/sex="male"
/tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr12"
/note="Vector: PAMP10; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
NIH."
ORIGIN
Query Match 33.6%; Score 30.2; DB 9; Length 225;
Best Local Similarity 60.2%; Pred. No. 3.4e+02;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

1 ATGAGAGTGAAGGAGGAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGCACCATG 60
|||||
212 AAGAGGAGGAGGAAGAACTGCCAGAAAGATGATGAGGAAGAGGAGGAGGAGGAGAGATG 153
|||||
61 CTCCTTGGGATGTTGATGTCG 83
|||||
152 ATGATGATGATGATGATGATG 130
|||||

RESULT 11
AA782068/c
LOCUS
DEFINITION
aa47d12.s1 Soares parathyroid tumor NDHPA Homo sapiens cDNA clone
1360127 3', similar to contains element MER28 repetitive element ;,
mRNA sequence.
AA782068
VERSION
AA782068.1 GI:2841399
KEYWORDS
EST.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 274)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

```

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1762 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 167.

FEATURES

source

1. 274
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1360127"
/tissue type="parathyroid tumor"
/dev stage="adult"
/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares parathyroid tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pTT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCCACCAATTTTTTTTTTTTTTTT-3']
to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 33.6%; Score 30.2; DB 9; Length 274;
Best Local Similarity 60.2%; Pred. No. 3.6e+02;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGAAGGAGAAATATCAGCATTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
Db 209 AAGAGGAGGAGAGAACTGCCAGAGATGATGAGGAAGAGGAGGAGGAGGAGAGATG 150
Qy 61 CTCCTTGGGATTTGATGATCTG 83
Db 149 ATGATGATGATGATGATGATG 127

RESULT 12
LOCUS AA932668 294 bp mRNA linear EST 07-JUL-1998
DEFINITION oo74a02.s1 NCI-CGAP GC4 Homo sapiens CDNA clone IMAGE:1571882 3' similar to contains element MBR28 repetitive element ;, mRNA sequence.
ACCESSION AA932668
VERSION AA932668.1 GI:3086633
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 294)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1155 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 164.

FEATURES

source

1. 294
Location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1571882"
/tissue type="pooled germ cell tumors"
/lab host="DH10B"
/clone lib="NCI CGAP GC4"
/note="Vector: pTT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 33.6%; Score 30.2; DB 9; Length 294;
Best Local Similarity 60.2%; Pred. No. 3.7e+02;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGAAGGAGAAATATCAGCATTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
Db 220 AAGAGGAGGAGGAGAACTGCCAGAGATGATGAGGAAGAGGAGGAGGAGGAGAGATG 161
Qy 61 CTCCTTGGGATTTGATGATCTG 83
Db 160 ATGATGATGATGATGATGATG 138

RESULT 13

BG986731/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

sequence tags

20202663

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

20202663

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MRI&t3=MK1-HT1183-040101-002-a06&t3=2001-01-04&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 24
 High quality sequence stop: 301.
 Location/Qualifiers

FEATURES

source

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 /note="Organ: head neck; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 33.6%; Score 30.2; DB 12; Length 301;
 Best Local Similarity 60.2%; Pred. No. 3.8e+02;
 Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 1 ATGAGAGTGAAGCAGAAATATCAGCTCTGGAGATGGGGTGGAGATGGGCACCATG 60
 Db 131 AAGAGAGAGGAGAGAACTGCCACCATGATGAGGAGAGGAGGAGGAGAGATG 72
 QY 61 CTCCTGGGATGTGATGATCTG 83
 Db 71 ATGATGATGATGATGATGATG 49

RESULT 14

AW788422/c
 LOCUS
 DEFINITION
 C00435-F Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
 cDNA clone C00435 similar to adenylyl cyclase-associated protein 2,
 mRNA sequence.

ACCESSION

AW788422

VERSION

AW788422.1

KEYWORDS

EST.

SOURCE

Blumeria graminis f. sp. hordei

ORGANISM

Blumeria graminis f. sp. hordei

REFERENCE

1 (bases 1 to 386)

AUTHORS

Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver, R.P.

TITLE

Gene identification in the fungal pathogen Blumeria graminis by

JOURNAL

expressed sequence tag analysis

COMMENT

Unpublished (2000)

Contact: Rasmussen, S.W.

Department of Yeast Genetics

Carlsberg Laboratory

10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark

Tel: 45 3327 5230

Fax: 45 3327 4766

Email: swr@crc.dk

High quality sequence stop: 386

POLYA=No.

Location/Qualifiers

1..386

/organism="Blumeria graminis f. sp. hordei"

/mol_type="mRNA"

/db_xref="taxon:62688"

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/cell_type="conidia"

/lab_host="Hordeum vulgare"

/clone_lib="Lambda Zap, Stratagene"

ORIGIN

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 Best Local Similarity 74.5%; Pred. No. 4.2e+02;
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 QY 24 GCACCTTGTGGAGATGGGGTGGAGATGGGGCACCACCATGCTCCTTGGGATGTT 74
 Db 289 GCCTGTGGGGTGGAGTGGTGGTGGGGCACAGTGCCCTTGGATTGTT 239

RESULT 15

AW789257/c

LOCUS

DEFINITION

AW789257
 C01016-F Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
 cDNA clone C01016 similar to adenylyl cyclase-associated protein 2,
 mRNA sequence.

ACCESSION

AW789257

VERSION

AW789257.1

KEYWORDS

EST.

SOURCE

Blumeria graminis f. sp. hordei

ORGANISM

Blumeria graminis f. sp. hordei

REFERENCE

1 (bases 1 to 400)

AUTHORS

Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver, R.P.

TITLE

Gene identification in the fungal pathogen Blumeria graminis by

JOURNAL

expressed sequence tag analysis

COMMENT

Unpublished (2000)

Contact: Rasmussen, S.W.

Department of Yeast Genetics

Carlsberg Laboratory

10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark

Tel: 45 3327 5230

Fax: 45 3327 4766

Email: swr@crc.dk

High quality sequence stop: 400

POLYA=No.

Location/Qualifiers

1..400

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/db_xref="taxon:62688"

/clone="C01016"

/cell_type="conidia"

/lab_host="Hordeum vulgare"

/clone_lib="Lambda Zap, Stratagene"

Search completed: March 11, 2004, 23:09:26

Job time : 1739.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:52:43 ; Search time 675.083 Seconds
(without alignments)
6934.037 Million cell updates/sec

Title: US-10-003-035-25

Perfect score: 108
Sequence: 1 tgtacaagaccacaacaa.....atatgagacaagcacattgt 108

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba:*
- 2: gb_hgt:*
- 3: gb_in:*
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- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rtd:*
- 36: em_htg_rtd:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	108	100.0	108	14	AY289013	AY289013 HIV-1 clo
2	108	100.0	108	14	HIVLAIAE	M64190 Human immun
3	108	100.0	108	14	HIVV3166	M61582 Human immun
4	108	100.0	108	14	HIVV3168	M61584 Human immun
5	108	100.0	108	14	HIVV3169	M61585 Human immun
6	108	100.0	108	14	HIVV3170	M61586 Human immun
7	108	100.0	108	14	HIVV3RE11	D78624 HIV-1 isola
8	108	100.0	108	14	HIVV3AA	M64768 Human immun
9	108	100.0	276	14	HIVLAIC21A	L48399 Human immun
10	108	100.0	288	6	I05601	I05601 Sequence 7
11	108	100.0	318	6	I05603	I05603 Sequence 9
12	108	100.0	405	14	HIVU40538	U40538 Human immun
13	108	100.0	405	14	HIVU40539	U40539 Human immun
14	108	100.0	423	6	I05605	I05605 Sequence 11
15	108	100.0	536	6	I05295	I05295 Sequence 5
16	108	100.0	537	6	I06664	I06664 Sequence 6
17	108	100.0	702	6	I05360	I05360 Sequence 10
18	108	100.0	1056	6	I05297	I05297 Sequence 6
19	108	100.0	1059	6	I06665	I06665 Sequence 7
20	108	100.0	1269	6	I06663	I06663 Sequence 5
21	108	100.0	1276	6	I05288	I05288 Sequence 4
22	108	100.0	1791	6	I06666	I06666 Sequence 8
23	108	100.0	1796	6	I05298	I05298 Sequence 7
24	108	100.0	1920	6	I05365	I05365 Sequence 13
25	108	100.0	2457	6	I05361	I05361 Sequence 11
26	108	100.0	2673	6	I05299	I05299 Sequence 8
27	108	100.0	2945	6	AR365081	AR365081 Sequence
28	108	100.0	8332	14	HIVRH102	M15654 Human immun
29	108	100.0	8933	6	AR094659	AR094659 Sequence
30	108	100.0	8933	6	AR382018	AR382018 Sequence
31	108	100.0	8933	6	AX078307	AX078307 Sequence
32	108	100.0	8933	6	AX078308	AX078308 Sequence
33	108	100.0	8933	6	AX078313	AX078313 Sequence
34	108	100.0	9213	6	E00987	E00987 Genomic DNA
35	108	100.0	9213	6	I04549	I04549 Sequence 11
36	108	100.0	9748	6	E01099	E01099 DNA sequenc
37	108	100.0	9748	14	REHTLV3	X01762 Human T-cel
38	108	100.0	9749	6	I07983	I07983 Sequence 1
39	108	100.0	9770	14	HIVPV22	K02083 Human immun
40	107	99.1	126	14	HIVCIAAA	M64773 Human immun
41	106.4	98.5	108	14	HIVLAIAE	M64195 Human immun
42	106.4	98.5	108	14	HIVLAIAE	M64196 Human immun
43	106.4	98.5	108	14	HIVLAIAE	M64198 Human immun
44	106.4	98.5	108	14	HIVLAIAH	M64219 Human immun
45	106.4	98.5	108	14	HIVLAIAJ	M64221 Human immun

ALIGNMENTS

RESULT 1
AY289013
LOCUS
DEFINITION
HIV-1 clone BAL#21 from USA envelope glycoprotein (env) gene,
partial cds.
ACCESSION
AY289013
VERSION
AY289013.1 GI:32264045
KEYWORDS
Human immunodeficiency virus 1 (HIV-1)
SOURCE
Human immunodeficiency virus 1
ORGANISM
Viruses; Retroviridae; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE
1 (bases 1 to 108)
Hoshino, Y., Tse, D.B., Rochford, G., Prabhakar, S., Hoshino S.,
Kuwabara, K., Ching, E., Raju, B., Gold, J.A., Borkowsky, W., Rom, W.N.,

QY 1 TGTACAGACCCCAACAAATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
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 Db 61 GCATTGTTTACATAGAAAAATAGGAATATGAGACAGCACATTGT 108

RESULT 4
 HIVV3168
 LOCUS
 DEFINITION Human immunodeficiency virus type 1 (HIV-1) envelope gene V3
 region, partial cds.
 ACCESSION M61584.1
 VERSION M61584.1 GI:329219
 KEYWORDS envelope-associated protein.
 SOURCE Human immunodeficiency virus 1 (HIV-1)
 ORGANISM Human immunodeficiency virus 1
 Viruses; Retrovirdae; Retroviridae; Lentivirus; Primate
 lentivirus group.
 REFERENCE 1 (bases 1 to 108)
 AUTHORS LaRosa,G.J., Davide,J.P., Weinhold,K., Waterbury,J.A., Profy,A.T.,
 Lewis,J.A., Langlois,A.J., Dreesman,G.R., Boswell,R.N.,
 Shaduck,P., Holley,L.H., Karplus,M., Bolognesi,D.P.,
 Matthews,T.J., Emini,E.A. and Putney,S.D.
 TITLE Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant
 JOURNAL Science 251 (4995), 811 (1991)
 MEDLINE 91361090
 PUBMED 1887238
 REFERENCE 2 (sites)
 AUTHORS LaRosa,G.J., Davide,J.P., Weinhold,K., Waterbury,J.A., Profy,A.T.,
 Lewis,J.A., Langlois,A.J., Dreesman,G.R., Boswell,R.N.,
 Shaduck,P., Holley,L.H., Karplus,M., Bolognesi,D.P.,
 Matthews,T.J., Emini,E.A. and Putney,S.D.
 TITLE Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant: corrections and clarifications
 JOURNAL Science 251 (4995), 811 (1991)
 MEDLINE 91118022
 PUBMED 1990444
 REFERENCE 3 (sites)
 AUTHORS LaRosa,G.J., Weinhold,K., Profy,A.T., Langlois,A.J., Dreesman,G.R.,
 Boswell,R.N., Shaduck,P., Bolognesi,D.P., Matthews,T.J.,
 Emini,E.A. and Putney,S.D.
 TITLE Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant: further clarifications
 JOURNAL Science 253 (5024), 1146 (1991)
 MEDLINE 91361090
 PUBMED 1887238
 COMMENT Original source text: Human immunodeficiency virus type 1 V3 region
 proviral DNA.

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 /db_xref="taxon:11676"
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QY 1 TGTACAGACCCCAACAAATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
 Db 1 TGTACAGACCCCAACAAATACAGAAAAAGTATCCGTATCCAGAGAGGACCCAGGAGA 60
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 Db 61 GCATTGTTTACATAGAAAAATAGGAATATGAGACAGCACATTGT 108

RESULT 5
 HIVV3169
 LOCUS
 DEFINITION Human immunodeficiency virus type 1 (HIV-1) envelope gene V3
 region, partial cds.
 ACCESSION M61585.1
 VERSION M61585.1 GI:329221
 KEYWORDS envelope-associated protein.
 SOURCE Human immunodeficiency virus 1 (HIV-1)
 ORGANISM Human immunodeficiency virus 1
 Viruses; Retrovirdae; Retroviridae; Lentivirus; Primate
 lentivirus group.
 REFERENCE 1 (bases 1 to 108)
 AUTHORS LaRosa,G.J., Davide,J.P., Weinhold,K., Waterbury,J.A., Profy,A.T.,
 Lewis,J.A., Langlois,A.J., Dreesman,G.R., Boswell,R.N.,
 Shaduck,P., Holley,L.H., Karplus,M., Bolognesi,D.P.,
 Matthews,T.J., Emini,E.A. and Putney,S.D.
 TITLE Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant
 JOURNAL Science 249 (4971), 932-935 (1990)
 MEDLINE 90364416
 PUBMED 2392685
 REFERENCE 2 (sites)
 AUTHORS LaRosa,G.J., Davide,J.P., Weinhold,K., Waterbury,J.A., Profy,A.T.,
 Lewis,J.A., Langlois,A.J., Dreesman,G.R., Boswell,R.N.,
 Shaduck,P., Holley,L.H., Karplus,M., Bolognesi,D.P.,
 Matthews,T.J., Emini,E.A. and Putney,S.D.
 TITLE Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant: corrections and clarifications
 JOURNAL Science 251 (4995), 811 (1991)
 MEDLINE 91118022
 PUBMED 1990444
 REFERENCE 3 (sites)
 AUTHORS LaRosa,G.J., Weinhold,K., Profy,A.T., Langlois,A.J., Dreesman,G.R.,
 Boswell,R.N., Shaduck,P., Bolognesi,D.P., Matthews,T.J.,
 Emini,E.A. and Putney,S.D.
 TITLE Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant: further clarifications
 JOURNAL Science 253 (5024), 1146 (1991)
 MEDLINE 91361090
 PUBMED 1887238
 COMMENT Original source text: Human immunodeficiency virus type 1 V3 region
 proviral DNA, sibling of 233.
 Location/Qualifiers
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 /organism="Human immunodeficiency virus 1"
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ORIGIN

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QY 1 TGTACAGAGCCCAACAACAAATACAGAAAAAGTATCCGTATCCAGAGAGGACCAGGAGA 60
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QY 61 GCATTTGTTTACAATAGGAAAAATAGGAAAAATAGGACAAAGCACATTGT 108
Db 61 GCATTTGTTTACAATAGGAAAAATAGGAAAAATAGGACAAAGCACATTGT 108

RESULT 6
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LOCUS Human immunodeficiency virus type 1 (HIV-1) envelope gene V3
DEFINITION region, partial cds.
ACCESSION M61586 M37586
VERSION M61586.1 GI:329223
KEYWORDS envelope-associated protein.
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
REFERENCE 1 (bases 1 to 108)
AUTHORS LaRosa,G.J., Davide,J.P., Weinhold,K., Waterbury,J.A., Profy,A.T.,
Lewis,J.A., Langlois,A.J., Dreesman,G.R., Boswell,R.N.,
Shaddock,P., Holley,L.H., Karplus,M., Bolognesi,D.P.,
Matthews,T.J., Emini,E.A. and Putney,S.D.
TITLE Conserved sequence and structural elements in the HIV-1 principal
neutralizing determinant
JOURNAL Science 249 (4971), 932-935 (1990)
MEDLINE 90364416
PUBMED 2392685
REFERENCE 2 (sites)
AUTHORS LaRosa,G.J., Davide,J.P., Weinhold,K., Waterbury,J.A., Profy,A.T.,
Lewis,J.A., Langlois,A.J., Dreesman,G.R., Boswell,R.N.,
Shaddock,P., Holley,L.H., Karplus,M., Bolognesi,D.P.,
Matthews,T.J., Emini,E.A. and Putney,S.D.
TITLE Conserved sequence and structural elements in the HIV-1 principal
neutralizing determinant: corrections and clarifications
JOURNAL Science 251 (4995), 811 (1991)
MEDLINE 91118022
PUBMED 1990444
REFERENCE 3 (sites)
AUTHORS LaRosa,G.J., Weinhold,K., Profy,A.T., Langlois,A.J., Dreesman,G.R.,
Boswell,R.N., Shaddock,P., Bolognesi,D.P., Matthews,T.J.,
Emeni,E.A. and Putney,S.D.
TITLE Conserved sequence and structural elements in the HIV-1 principal
neutralizing determinant: further clarifications
JOURNAL Science 253 (5024), 1146 (1991)
MEDLINE 91361090
PUBMED 1887238
COMMENT Original DNA, sibling of 153 and 185.
FEATURES
source
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Best Local Similarity 100.0%; Pred. No. 4.5e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGAGCCCAACAACAAATACAGAAAAAGTATCCGTATCCAGAGAGGACCAGGAGA 60
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Db 61 GCATTTGTTTACAATAGGAAAAATAGGAAAAATAGGACAAAGCACATTGT 108

RESULT 7
HIVV3RE11
LOCUS HIV-1 isolate No.5 env gene, V3 region, partial cds.
DEFINITION
ACCESSION D78624
VERSION D78624.1 GI:17855501
KEYWORDS env.
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
REFERENCE 1 (sites)
AUTHORS Kakizawa,J., Ushijima,H., Morishita,Y., Oka,S., Ikeda,Y. and
Muller,W.E.
TITLE Diversity of HIV type 1 envelope V3 loop region in saliva
JOURNAL AIDS Res. Hum. Retroviruses 12 (6), 561-563 (1996)
MEDLINE 96296970
PUBMED 8679313
REFERENCE 2 (bases 1 to 108)
AUTHORS Kakizawa,J., Ushijima,H., Morishita,Y., Oka,S., Ikeda,Y. and
Muller,W.E.
TITLE Diversity of HIV Type 1 Envelope V3 Loop Region in Saliva
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 108)
AUTHORS Ushijima,H.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1995) Hiroshi Ushijima, The University of Tokyo,
Faculty of Medicine, Department of Maternal and Child Health; Hongo
7-3-1, Bunkyo-Ku, Tokyo 113, Japan
(E-mail:ushijima@u-tokyo.ac.jp, Tel:+81-3-3812-2111(ex.3515),
Fax:+81-3-5802-2961)
COMMENT On Jan 18, 1997 this sequence version replaced gi:1122714.
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ORIGIN
Query Match 100.0%; Score 108; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.5e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGAGCCCAACAACAAATACAGAAAAAGTATCCGTATCCAGAGAGGACCAGGAGA 60
Db 1 TGTACAGAGCCCAACAACAAATACAGAAAAAGTATCCGTATCCAGAGAGGACCAGGAGA 60

QY 61 GCATTTGTTTACAATAGGAAAAATAGGAAAAATAGGACAAAGCACATTGT 108
Db 61 GCATTTGTTTACAATAGGAAAAATAGGAAAAATAGGACAAAGCACATTGT 108

RESULT 8
HIVV3RE11
LOCUS HIV-1 isolate No.5 env gene, V3 region, partial cds.
DEFINITION
ACCESSION D78624
VERSION D78624.1 GI:17855501
KEYWORDS env.
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
REFERENCE 1 (sites)
AUTHORS Kakizawa,J., Ushijima,H., Morishita,Y., Oka,S., Ikeda,Y. and
Muller,W.E.
TITLE Diversity of HIV type 1 envelope V3 loop region in saliva
JOURNAL AIDS Res. Hum. Retroviruses 12 (6), 561-563 (1996)
MEDLINE 96296970
PUBMED 8679313
REFERENCE 2 (bases 1 to 108)
AUTHORS Kakizawa,J., Ushijima,H., Morishita,Y., Oka,S., Ikeda,Y. and
Muller,W.E.
TITLE Diversity of HIV Type 1 Envelope V3 Loop Region in Saliva
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 108)
AUTHORS Ushijima,H.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1995) Hiroshi Ushijima, The University of Tokyo,
Faculty of Medicine, Department of Maternal and Child Health; Hongo
7-3-1, Bunkyo-Ku, Tokyo 113, Japan
(E-mail:ushijima@u-tokyo.ac.jp, Tel:+81-3-3812-2111(ex.3515),
Fax:+81-3-5802-2961)
COMMENT On Jan 18, 1997 this sequence version replaced gi:1122714.
FEATURES
source
1..108
/organism="Human immunodeficiency virus 1"
/mol_type="genomic RNA"
/isolates="No.5"
/db_xref="taxon:11676"
/clone="A-1"
1..105
/gene="env"
<1..>105
/gene="env"
/notes="V3 region"
/codon_start=1
/protein_id="BAA11444.1"
/db_xref="GI:1122715"
/translation="CTRPNNNTRKSIRIQGPGRAFVTIGKIGNRQAH"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.5e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGAGCCCAACAACAAATACAGAAAAAGTATCCGTATCCAGAGAGGACCAGGAGA 60
Db 1 TGTACAGAGCCCAACAACAAATACAGAAAAAGTATCCGTATCCAGAGAGGACCAGGAGA 60

QY 61 GCATTTGTTTACAATAGGAAAAATAGGAAAAATAGGACAAAGCACATTGT 108
Db 61 GCATTTGTTTACAATAGGAAAAATAGGAAAAATAGGACAAAGCACATTGT 108

RESULT 8

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HIVC3AA          126 bp ss-RNA      linear      VRL 02-AUG-1993
LOCUS            Human immunodeficiency virus type 1 envelope gene V3 region,
DEFINITION       partial cds.
ACCESSION        M64768
VERSION          GI:326450
KEYWORDS         envelope-associated protein.
SOURCE           Human immunodeficiency virus 1 (HIV-1)
ORGANISM         Human immunodeficiency virus 1
REFERENCE        1 (bases 1 to 126)
AUTHORS          Nara, P.L., Smith, L., Dunlop, N., Hatch, W., Merges, M., Waters, D.,
                  Kellier, J., Gallo, R.C., Fischinger, P.J., and Goudsmit, J.
TITLE            Emergence of viruses resistant to neutralization by V3-specific
                  antibodies in experimental human immunodeficiency virus type 1 IIIB
                  infection of chimpanzees
JOURNAL          J. Virol. 64 (8), 3779-3791 (1990)
MEDLINE          90317876
PUBMED          2370681
COMMENT          Original source text: Human immunodeficiency virus type 1 (strain
                  IIIB/H9)
FEATURES         source
                  1..126
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Query Match      100.0%; Score 108; DB 14; Length 126;
Best Local Similarity 100.0%; Pred. No. 4.4e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTACAGACCCCAACAATACAGAAAAAGTAGTCCGTATCCAGAGAGGACGAGGAGA 60
DB 19 TGTACAGACCCCAACAATACAGAAAAAGTAGTCCGTATCCAGAGAGGACGAGGAGA 78
OY 61 GCATTGTGTACAAATAGGAAAAATAGAAATATGAGACAGACGACATTGT 108
DB 79 GCATTGTGTACAAATAGGAAAAATAGAAATATGAGACAGACGACATTGT 126

RESULT 9
HIVLAC21A        276 bp ss-RNA      linear      VRL 11-APR-1996
LOCUS            Human immunodeficiency virus type 1 (isolate LARC21) envelope
DEFINITION       glycoprotein gp120 (env) gene, V3 region.
ACCESSION        L48399
VERSION          GI:1049695
KEYWORDS         envelope glycoprotein; variable domain III.
SOURCE           Human immunodeficiency virus 1 (HIV-1)
ORGANISM         Human immunodeficiency virus 1
REFERENCE        1 (bases 1 to 276)
AUTHORS          Wain-Hobson, S., Sonigo, P., Danos, O., Cole, S. and Allison, M.
TITLE            Nucleotide sequence of the AIDS virus, LAV
JOURNAL          Cell 40 (1), 9-17 (1985)
MEDLINE          85099333
PUBMED          2981635
REFERENCE        2 (bases 1 to 276)
AUTHORS          Muesing, M.A., Smith, D.H., Cabradilla, C.D., Benton, C.V., Lasky, L.A.
                  and Capon, D.J.
TITLE            Nucleic acid structure and expression of the human
                  AIDS/lymphadenopathy retrovirus

Query Match      100.0%; Score 108; DB 14; Length 126;
Best Local Similarity 100.0%; Pred. No. 4.4e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTACAGACCCCAACAATACAGAAAAAGTAGTCCGTATCCAGAGAGGACGAGGAGA 60
DB 19 TGTACAGACCCCAACAATACAGAAAAAGTAGTCCGTATCCAGAGAGGACGAGGAGA 78
OY 61 GCATTGTGTACAAATAGGAAAAATAGAAATATGAGACAGACGACATTGT 108
DB 79 GCATTGTGTACAAATAGGAAAAATAGAAATATGAGACAGACGACATTGT 126

RESULT 9
HIVLAC21A        276 bp ss-RNA      linear      VRL 11-APR-1996
LOCUS            Human immunodeficiency virus type 1 (isolate LARC21) envelope
DEFINITION       glycoprotein gp120 (env) gene, V3 region.
ACCESSION        L48399
VERSION          GI:1049695
KEYWORDS         envelope glycoprotein; variable domain III.
SOURCE           Human immunodeficiency virus 1 (HIV-1)
ORGANISM         Human immunodeficiency virus 1
REFERENCE        1 (bases 1 to 276)
AUTHORS          Wain-Hobson, S., Sonigo, P., Danos, O., Cole, S. and Allison, M.
TITLE            Nucleotide sequence of the AIDS virus, LAV
JOURNAL          Cell 40 (1), 9-17 (1985)
MEDLINE          85099333
PUBMED          2981635
REFERENCE        2 (bases 1 to 276)
AUTHORS          Muesing, M.A., Smith, D.H., Cabradilla, C.D., Benton, C.V., Lasky, L.A.
                  and Capon, D.J.
TITLE            Nucleic acid structure and expression of the human
                  AIDS/lymphadenopathy retrovirus

JOURNAL          Nature 313 (6002), 450-458 (1985)
MEDLINE          85111157
PUBMED          2982104
REFERENCE        3 (bases 1 to 276)
AUTHORS          Wain-Hobson, S., Vartanian, J.-P., Henry, M., Chenciner, N.,
                  Cheynier, R., Delassus, S., Martins, L.P., Sala, M., Nugyre, M.-T.,
                  Guetard, D., Klatzmann, D., Gluckman, J.-C., Rozenbaum, W.,
                  Barre-Sinoussi, F. and Montagnier, L.
TITLE            LAV revisited: origins of the early HIV-1 isolates from Institut
                  Pasteur
JOURNAL          Science 252 (5008), 961-965 (1991)
MEDLINE          91240282
PUBMED          2035026
REFERENCE        4 (bases 1 to 276)
AUTHORS          Lukashov, V.V. and Goudsmit, J.
TITLE            Increasing genotypic and phenotypic selection from the original
                  genomic RNA populations of HIV-1 strains LAI and MN (NM) by
                  peripheral blood mononuclear cell culture, B-cell-line propagation
                  and T-cell-line adaptation
JOURNAL          AIDS 9 (12), 1307-1311 (1995)
MEDLINE          96188304
PUBMED          8605049
COMMENT          Original source text: Human immunodeficiency virus type 1
                  (individual isolate Patient LAI) cDNA to genomic RNA.
FEATURES         source
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                  1..276
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                  /db_xref="GI:1128994"
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Query Match      100.0%; Score 108; DB 14; Length 276;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTACAGACCCCAACAATACAGAAAAAGTAGTCCGTATCCAGAGAGGACGAGGAGA 60
DB 79 TGTACAGACCCCAACAATACAGAAAAAGTAGTCCGTATCCAGAGAGGACGAGGAGA 138
OY 61 GCATTGTGTACAAATAGGAAAAATAGGAAATATGAGACAGACGACATTGT 108
DB 139 GCATTGTGTACAAATAGGAAAAATAGGAAATATGAGACAGACGACATTGT 186

RESULT 10
I05601           288 bp      DNA      linear      PAT 02-DEC-1994
LOCUS            Sequence 7 from Patent EP 0306219.
DEFINITION       I05601
ACCESSION        I05601
KEYWORDS         I05601.1 GI:590566
SOURCE           Unknown.
ORGANISM         Unclassified.
REFERENCE        1 (bases 1 to 288)
AUTHORS          Rusche, J.R., Putney, S.D., Javaherian, K., Farley, J., Grimala, R.,
                  Lynn, D., Petro, J. and O'Keefe, T.
TITLE            Novel HIV proteins and peptides useful in the diagnosis,
                  prophylaxis or therapy of AIDS
JOURNAL          Patent: EP 0306219-A2 7 08-MAR-1989;
FEATURES         Location/Qualifiers

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Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGAGCCCAACACATACAGAAAGATATCGGTATCCAGAGAGGACGAGGAGA 60
DB 115 TGTACAGAGCCCAACACATACAGAAAGATATCGGTATCCAGAGAGGACGAGGAGA 174

QY 61 GCATTTGTTACATAGGAAATAGGAAATATGAGCAAGCATTGT 108
DB 175 GCATTTGTTACATAGGAAATAGGAAATATGAGCAAGCATTGT 222

RESULT 11
LOCUS I05603 318 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 9 from Patent EP 0306219.
ACCESSION I05603
VERSION I05603.1 GI:590567
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 318)
AUTHORS Rusche,J.R., Putney,S.D., Javaherian,K., Farley,J., Grimaila,R.,
Lynn,D., Petro,J. and O'Keefe,T.
TITLE Novel HIV proteins and peptides useful in the diagnosis,
prophylaxis or therapy of AIDS
JOURNAL Patent: EP 0306219-A2, 9 08-MAR-1989;
FEATURES
Location/Qualifiers
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Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 25 TGTACAGAGCCCAACACATACAGAAAGATATCGGTATCCAGAGAGGACGAGGAGA 84

QY 61 GCATTTGTTACATAGGAAATAGGAAATATGAGCAAGCATTGT 108
DB 85 GCATTTGTTACATAGGAAATAGGAAATATGAGCAAGCATTGT 132

RESULT 12
LOCUS HIVU40538 405 bp DNA linear VRL 12-OCT-1996
DEFINITION Human immunodeficiency virus type 1 isolate D22/428 envelope
glycoprotein gp120 (env) gene, c2v3 region, partial cds.
ACCESSION U40538
VERSION U40538.1 GI:1620476
KEYWORDS
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE 1 (bases 1 to 405)
AUTHORS Quinones-Mateu,M.E., Holguin,A., Soriano,V. and Domingo,E.
TITLE env gene diversity of HIV type 1 isolates from Spain
JOURNAL AIDS Res. Hum. Retroviruses 12 (10), 955-957 (1996)
MEDLINE 96392169
PUBMED 8798981
REFERENCE 2 (bases 198 to 331)
AUTHORS Quinones-Mateu,M.E., Holguin,A., Dopazo,J., Najera,I. and
Domingo,E.
TITLE Point mutant frequencies in the pol gene of human immunodeficiency
virus type 1 are two- to threefold lower than those of env
JOURNAL AIDS Res. Hum. Retroviruses 12 (12), 1117-1128 (1996)

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Domingo,E.
Point mutant frequencies in the pol gene of human immunodeficiency
virus type 1 are two- to threefold lower than those of env
JOURNAL AIDS Res. Hum. Retroviruses 12 (12), 1117-1128 (1996)
MEDLINE 97000986
PUBMED 8844016
REFERENCE 3 (bases 1 to 405)
AUTHORS Quinones-Mateu,M.E.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-1995) Miguel E. Quinones-Mateu, Centro de
Biología Molecular Severo Ochoa, Universidad Autónoma de Madrid,
Cantoblanco, Madrid, 28049, Spain
COMMENT On Oct 16, 1996 this sequence version replaced gi:1304535.
FEATURES
Location/Qualifiers
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/cell_type="peripheral blood lymphocytes"
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gene

CDS

ORIGIN

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DB 298 TGTACAGAGCCCAACACATACAGAAAGATATCGGTATCCAGAGAGGACGAGGAGA 357

QY 61 GCATTTGTTACATAGGAAATAGGAAATATGAGCAAGCATTGT 108
DB 358 GCATTTGTTACATAGGAAATAGGAAATATGAGCAAGCATTGT 405

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RESULT 13

HIVU40539

LOCUS

DEFINITION

Human immunodeficiency virus type 1 (HIV-1)

glycoprotein gp120 (env) gene, c2v3 region, partial cds.

U40539.1 GI:1620477

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human immunodeficiency virus 1 (HIV-1)

Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate

lentivirus group.

1 (bases 1 to 405)

Quinones-Mateu,M.E., Holguin,A., Soriano,V. and Domingo,E.

env gene diversity of HIV type 1 isolates from Spain

AIDS Res. Hum. Retroviruses 12 (10), 955-957 (1996)

96392169

8798981

REFERENCE

AUTHORS

Quinones-Mateu,M.E., Holguin,A., Dopazo,J., Najera,I. and

Domingo,E.

Point mutant frequencies in the pol gene of human immunodeficiency

virus type 1 are two- to threefold lower than those of env

AIDS Res. Hum. Retroviruses 12 (12), 1117-1128 (1996)

JOURNAL

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MEDLINE 97000986
PUBMED 8844016
REFERENCE 3 (bases 1 to 405)
AUTHORS Quinones-Mateu,M.E.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-1995) Miguel E. Quinones-Mateu, Centro de
Biologia Molecular 'Severo Ochoa', Universidad Autonoma de Madrid,
Cantoblanco, Madrid, 28049, Spain
COMMENT On Oct 16, 1996 this sequence version replaced gi:1304537.
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/cell_type="peripheral blood lymphocytes"
1..405
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<1..>405
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/protein_id="AAC55850.1"
/db_xref="GI:1304538"
/translation="NTSVITQACPKVSEPIPIHVCAPAGPAILKCNKNTFNGTGPCT
NVSTVQCTHGIRPVYSTQLLNGSLAEVEVIRSANFTDNARTIIVQLNQSVINCTR
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.2e-20;
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DB 298 TGTACAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGCCAGGGAGA 357

QY 61 GCATTTGTTACAAATAGGAAAAATAGGAAATATGAGACAAGCACATTGT 108
DB 358 GCATTTGTTACAAATAGGAAAAATAGGAAATATGAGACAAGCACATTGT 405

RESULT 14
I05605
LOCUS 423 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 11 from Patent EP 0306219.
ACCESSION I05605
VERSION I05605.1 GI:590568
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 423)
AUTHORS Rusche,J.R., Putney,S.D., Javaherian,K., Farley,J., Grimalia,R.,
Lynn,D., Petro,J. and O'Keefe,T.
TITLE Novel HIV proteins and polypeptides useful in the diagnosis,
prophylaxis or therapy of AIDS
JOURNAL Patent: EP 0306219-A2 11 08-MAR-1989;
FEATURES
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGCCAGGGAGA 60

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DB 115 TGTACAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGCCAGGGAGA 174
QY 61 GCATTTGTTACAAATAGGAAAAATAGGAAATATGAGACAAGCACATTGT 108
DB 175 GCATTTGTTACAAATAGGAAAAATAGGAAATATGAGACAAGCACATTGT 222

RESULT 15
I05295
LOCUS 536 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent EP 0255190.
ACCESSION I05295
VERSION I05295.1 GI:591127
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 536)
AUTHORS Putney,S.D., Lynn,D., Javaherian,K., Mueller,Wt. and Farley,J.
TITLE Recombinant polypeptides and their uses, including assay for aids
virus
JOURNAL Patent: EP 0255190-A2 5 03-FEB-1988;
FEATURES
source
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Location/Qualifiers
/organism="unknown"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGCCAGGGAGA 60
DB 25 TGTACAGACCCCAACAATACAGAAAAAGTATCCGTATCCAGAGAGCCAGGGAGA 84

QY 61 GCATTTGTTACAAATAGGAAAAATAGGAAATATGAGACAAGCACATTGT 108
DB 85 GCATTTGTTACAAATAGGAAAAATAGGAAATATGAGACAAGCACATTGT 132

Search completed: March 11, 2004, 21:24:04
Job time : 680.083 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:51:27 ; Search time 304.156 Seconds
(without alignment)
1801.765 Million cell updates/sec

Title: US-10-003-035-75

Perfect score: 129

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Scoring table: IDENTITY_NUC

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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	129	100.0	129	9 ADB87802	AdB87802 gp41 tran
2	129	100.0	129	9 ADB66326	AdB66326 HIV gp41
3	129	100.0	615	9 ADB87771	AdB87771 HIV-1 p17
4	129	100.0	615	9 ADB66293	AdB66293 HIV p17 m
5	129	100.0	915	9 ADB87777	AdB87777 HIV-1 p24
6	129	100.0	915	9 ADB66229	AdB66229 HIV p24 m
7	129	100.0	1026	2 AAQ03968	AAQ03968 PENV9 enc
8	129	100.0	1026	2 AAQ03968	AAQ03968 PENV9 enc
9	129	100.0	1308	9 ADB87765	AdB87765 HIV-1 p17
10	129	100.0	1308	9 ADB66287	AdB66287 HIV p17/2
11	129	100.0	2237	1 AAN90531	AAN90531 Sequence
12	129	100.0	2280	9 ADB87745	AdB87745 HIV-1 str
13	129	100.0	2280	9 ADB66267	AdB66267 HIV clone
14	129	100.0	2553	1 AAN80949	AAN80949 HIV prote
15	129	100.0	2583	9 ADB87753	AdB87753 HIV-1 BHL
16	129	100.0	2583	9 ADB66275	AdB66275 HIV E m/E
17	129	100.0	2747	9 ADB87752	AdB87752 HIV-1 BHL
18	129	100.0	2747	9 ADB66274	AdB66274 HIV E mde
19	129	100.0	2945	2 AAT05127	AAT05127 HIV virus
20	129	100.0	2950	9 ADB87751	AdB87751 HIV-1 BHL
21	129	100.0	2950	9 ADB66273	AdB66273 HIV E mde
22	129	100.0	3156	1 AAN60128	AAN60128 Sequence
23	129	100.0	3157	9 ADB87743	AdB87743 HIV-1 str

ALIGNMENTS

RESULT 1

ADB87802

ID ADB87802 standard; DNA; 129 BP.

XX ADB87802;

XX ADB87802;

DT 04-DEC-2003 (first entry)

XX

DE gp41 transmembrane domain DNA.

XX

adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
antiparasitic; protozoicide; cytostatic; immunomodulatory; vaccine;
pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.

OS Human immunodeficiency virus 1.

XX

PN US2002155127-A1.

XX

PD 24-OCT-2002.

XX

PF 01-NOV-2001; 2001US-00003035.

XX

PR 02-JUN-2000; 2000US-00585599.

XX

PR 04-JUN-2001; 2001WO-US018238.

XX

PA (WANG/) WANG D.

XX

PI Wang D;

XX

DR WPI; 2003-182621/18.

XX

PT New recombinant adenoviruses, useful as vaccines for eliciting immune
response or conferring protection against infection of a pathogenic
antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
antigens.

XX

PS Claim 24; Page 81; 156pp; English.

XX

CC This invention describes a novel recombinant adenovirus comprising an HIV
sequence encoding an HIV antigen, where expression of the HIV antigen by
the recombinant adenovirus elicits an immune response directed against
the HIV antigen in a host upon infection of the host by the recombinant
adenovirus. The products of the invention have anti-HIV, virucide,
antibacterial, antiparasitic, cytostatic and
immunomodulatory activity. The recombinant adenoviruses are useful as
vaccines for eliciting immune response or conferring protection against


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CC  Invention.
XX  Sequence 615 BP; 217 A; 101 C; 162 G; 135 T; 0 U; 0 Other;
SQ  Query Match
    Best Local Similarity 100.0%; Score 129; DB 9; Length 615;
    Best Local Similarity 100.0%; Pred. No. 1.6e-30;
    Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TTATTCAATAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTCGTGACTTTCT 60
DB  484 TTATTCAATAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTCGTGACTTTCT 543

QY  61 GTAGTGAATAGTAGGAGGAGGATATTCACCAATTATCGTTTCAGACCCACCTCCCAATC 120
DB  544 GTAGTGAATAGTAGGAGGAGGATATTCACCAATTATCGTTTCAGACCCACCTCCCAATC 603

QY  121 CCGAGGGGA 129
DB  604 CCGAGGGGA 612

RESULT 4
ADD66293
ID  ADD66293 standard; DNA; 615 BP.
AC  ADD66293;
DT  15-JAN-2004 (first entry)
XX  HIV p17 membrane form DNA.
XX  virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;
XX  infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
XX  respiratory syncytial virus; herpes simplex virus; human papilloma virus;
XX  HIV infection; ds; Gene.
XX  Human immunodeficiency virus.
XX  US2003138459-A1.
XX  24-JUL-2003.
XX  17-MAR-2003; 2003US-00286332.
XX  02-JUN-2000; 2000US-00585599.
XX  04-JUN-2001; 2001WO-US018238.
XX  01-NOV-2001; 2001US-00003035.
XX  (WANG/) WANG D.
XX  Wang D;
XX  WPI; 2003-851718/79.
XX  P-PSDB; ADD66296.
XX  Enhancing the immunity of a host to infection of a first and second
XX  pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or
XX  HIV infections comprising administering to the host a first and a second
XX  recombinant adenovirus.
XX  Example; SEQ ID NO 42; 185pp; English.
XX  The invention relates to a method of enhancing the immunity of a host to
XX  infection of a first and second pathogenic virus comprising administering
XX  to the host a first and a second recombinant adenovirus. The method is
XX  useful for enhancing immunity of the host to infections, e.g. influenza,
XX  Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes
XX  simplex or human papilloma virus or HIV infections. The present sequence
XX  is used in the exemplification of the invention.
XX  Sequence 615 BP; 217 A; 101 C; 162 G; 135 T; 0 U; 0 Other;
SQ  Query Match
    Best Local Similarity 100.0%; Score 129; DB 9; Length 615;
    Best Local Similarity 100.0%; Pred. No. 1.6e-30;
    Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TTATTCAATAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTCGTGACTTTCT 60
DB  484 TTATTCAATAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTCGTGACTTTCT 543

QY  61 GTAGTGAATAGTAGGAGGAGGATATTCACCAATTATCGTTTCAGACCCACCTCCCAATC 120
DB  544 GTAGTGAATAGTAGGAGGAGGATATTCACCAATTATCGTTTCAGACCCACCTCCCAATC 603

QY  121 CCGAGGGGA 129
DB  604 CCGAGGGGA 612

RESULT 5
ADD87777
ID  ADD87777 standard; DNA; 915 BP.
XX  ADD87777;
XX  AC  ADD87777;
XX  DT  04-DEC-2003 (first entry)
XX  DE  HIV-1 p24 membrane form DNA SEQ ID 48.
XX  KW  adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
XX  KW  antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;
XX  KW  pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
XX  OS  Human immunodeficiency virus 1.
XX  US2002155127-A1.
XX  24-OCT-2002.
XX  01-NOV-2001; 2001US-00003035.
XX  02-JUN-2000; 2000US-00585599.
XX  04-JUN-2001; 2001WO-US018238.
XX  (WANG/) WANG D.
XX  Wang D;
XX  WPI; 2003-182621/18.
XX  New recombinant adenoviruses, useful as vaccines for eliciting immune
XX  response or conferring protection against infection of a pathogenic
XX  antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
XX  antigens.
XX  Claim 30; Page 63; 156pp; English.
XX  This invention describes a novel recombinant adenovirus comprising an HIV
XX  sequence encoding an HIV antigen, where expression of the HIV antigen by
XX  the recombinant adenovirus elicits an immune response directed against
XX  the HIV antigen in a host upon infection of the host by the recombinant
XX  adenovirus. The products of the invention have anti-HIV, virucide,
XX  antibacterial, antiparasitic, protozoacide, cytostatic and
XX  immunomodulatory activity. The recombinant adenoviruses are useful as
XX  vaccines for eliciting immune response or conferring protection against
XX  infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B,
XX  C, D or E or tumour antigens. The recombinant adenoviruses are also
XX  useful as genetic vaccines against pathogenic bacteria, parasites or
XX  protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing
XX  the immunogenicity of the HIV antigens. This sequence represents an HIV-1
XX  strain BH10 antigen construct described in the disclosure of the
XX  invention.
XX  Sequence 915 BP; 314 A; 168 C; 229 G; 204 T; 0 U; 0 Other;
SQ  Query Match
    Best Local Similarity 100.0%; Score 129; DB 9; Length 915;
    Best Local Similarity 100.0%; Pred. No. 1.6e-30;
    Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 1.8e-30; Mismatches 0; Indels 0; Gaps 0;

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTCAATATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 60

Db 784 TTATTCAATATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 843

QY 61 GTAGTGAATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 120

Db 844 GTAGTGAATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 903

QY 121 CCGAGGGGA 129

Db 904 CCGAGGGGA 912

RESULT 6

ADD66299

ID ADD66299 standard; DNA; 915 BP.

XX AC

XX ADD66299;

DT 15-JAN-2004 (first entry)

DE HIV p24 membrane form DNA.

DE virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;

KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;

KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;

KW HIV infection; ds; gene.

XX Human immunodeficiency virus.

OS US2003138459-A1.

XX 24-JUL-2003.

XX 17-MAR-2003; 2003US-00286332.

XX 02-JUN-2000; 2000US-00585559.

PR 04-JUN-2001; 2001WO-US018238.

PR 01-NOV-2001; 2001US-00003035.

XX (WANG/) WANG D.

PA Wang D;

PI WPI; 2003-851718/79.

DR P-PSDB; ADD66302.

XX Enhancing the immunity of a host to infection of a first and second

PT pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or

PT HIV infections comprises administering to the host a first and a second

PT recombinant adenovirus.

XX Example; SEQ ID NO 48; 185pp; English.

PS The invention relates to a method of enhancing the immunity of a host to

CC infection of a first and second pathogenic virus comprising administering

CC to the host a first and a second recombinant adenovirus. The method is

CC useful for enhancing immunity of the host to infections, e.g. influenza,

CC Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes

CC simplex or human papilloma virus or HIV infections. The present sequence

CC is used in the exemplification of the invention.

XX Sequence 915 BP; 314 A; 168 C; 229 G; 204 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 129; DB 9; Length 915;

Best Local Similarity 100.0%; Pred. No. 1.8e-30;

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTCAATATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 60

Db 784 TTATTCAATATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 843

QY 61 GTAGTGAATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 120

Db 844 GTAGTGAATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 903

QY 121 CCGAGGGGA 129

Db 904 CCGAGGGGA 912

RESULT 7

AAQ03968

ID AAQ03968 standard; DNA; 1026 BP.

XX AC

XX AAQ03968;

DT 04-SEP-1990 (first entry)

DE pENV9 encoding a recombinant peptide with HIV antigenicity.

DE human immunodeficiency virus; antigenicity; gp120; gp41; poliovirus.

KW Synthetic.

OS US4861707-A.

PN 29-AUG-1989.

PD 02-FEB-1987; 87US-00010056.

PF 02-FEB-1987; 87US-00010056.

PR 02-FEB-1987; 87US-00010056.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PA Ivanoff LA, Petteway SR;

PI WPI; 1990-122902/16.

DR P-PSDB; AAR04019.

XX Recombinant peptide with antigenicity of human immuno-deficiency virus -

PT comprises forty-six amino acids from gp. 120 C-terminal and two hundred

PT and forty amino acids from gp. 41 N-terminal.

XX Claim 1; Fig 4; 13pp; English.

PS The sequence encodes ENV9, a recombinant peptide. ENV9 consists of about

CC 54 amino acids from the N-terminal of a poliovirus sequence (pEXC), as

CC well as those regions of HIV gp120 and gp41 detailed above. ENV9 can be

CC used to detect HIV antibodies. "False positive" results are minimised as

CC it contains few non-critical antigens. It can also be used in a vaccine

CC against HIV

XX Sequence 1026 BP; 335 A; 178 C; 275 G; 238 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 129; DB 2; Length 1026;

Best Local Similarity 100.0%; Pred. No. 1.8e-30;

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTCAATATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 60

Db 820 TTATTCAATATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 879

QY 61 GTAGTGAATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 120

Db 880 GTAGTGAATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 939

QY 121 CCGAGGGGA 129

Db 940 CCGAGGGGA 948

RESULT 8

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AAQ28095
ID AAQ28095 standard; DNA; 1026 BP.
XX AC
XX AAQ28095;
XX DT
XX 25-MAR-2003 (revised)
XX 12-FEB-1993 (first entry)
XX DE
XX Recombinant DNA encoding ENV9.
XX KW
XX Poliovirus; HIV; human immunodeficiency virus; AIDS; gp120; gp41; ss.
XX OS
XX Synthetic.
XX PN
XX US5141867-A.
XX PD
XX 25-AUG-1992.
XX PF
XX 04-MAY-1989; 89US-00347004.
XX PR
XX 02-FEB-1987; 87US-00010056.
XX PA
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI
XX Ivanoff LA, Petteway SR;
XX DR
XX WPI; 1992-307861/37.
XX PR
XX P-PSDB; AAR26787.
XX PT
XX Nucleotide sequence encoding a HIV antigen - comprising the C-terminal
XX region of Gp120 and N-terminal of Gp41. for use in diagnosis and in
XX vaccines.
XX PS
XX Claim 3; Fig 4; 12pp; English.
XX CC
XX The plasmid pENV9 was constructed by ligating the BglII/BamHI fragment
XX (nt 7196-8053) of HIV clone lambda BH10 with the BglII/ BamHI vector
XX fragment of pEXC. The prod. was used to transform E. coli strain HB101
XX and MM294. The transformants produced a protein ENV9 contg. 349 amino
XX acids corresp. to 54 amino acids from the N- terminal of the poliovirus
XX sequence of pEXC, 46 amino acids of the C- terminal of the gp120 domain
XX and 240 amino acids of the N-terminal of the gp41 domain. The peptide
XX comprises the early detection antigen from gp120 and a highly reactive
XX antigen from gp41 thus providing broad sensitivity to HIV antibodies. The
XX sensitivity of the peptides permits the detection of HIV infection using
XX small ams. of diagnostic reagents. The peptides have improved stability
XX as compared to larger antigenic segments and contain fewer noncritical
XX antigens which minimises the possibility of false positive results in
XX detection of HIV infection. The peptides can also be used in vaccines
XX protective against HIV. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ
XX Sequence 1026 BP; 335 A; 178 C; 275 G; 238 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 129; DB 2; Length 1026;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-30;
XX Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTATTCAATAGTAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTCGTGACTTTCT 60
Db 820 TTATTCAATAGTAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTCGTGACTTTCT 879
QY 61 GTAGTGAATAGTAGGAGGAGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 120
Db 880 GTAGTGAATAGTAGGAGGAGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 939
QY 121 CCGAGGGGA 129
Db 940 CCGAGGGGA 948
RESULT 9
ADB87765
ID ADB87765 standard; DNA; 1308 BP.
XX AC
XX ADB87765;
XX DT
XX 04-DEC-2003 (first entry)
XX DE
XX HIV-1 p17/24 membrane form DNA SEQ ID 36.
XX KW
XX adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
XX antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;
XX pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
XX OS
XX Human immunodeficiency virus 1.
XX PN
XX US2002155127-A1.
XX PD
XX 24-OCT-2002.
XX PF
XX 01-NOV-2001; 2001US-00003035.
XX PR
XX 02-JUN-2000; 2000US-00585599.
XX PR
XX 04-JUN-2001; 2001WO-US018238.
XX PA
XX (WANG/) WANG D.
XX PI
XX Wang D;
XX DR
XX WPI; 2003-182621/18.
XX PT
XX New recombinant adenoviruses, useful as vaccines for eliciting immune
XX response or conferring protection against infection of a pathogenic
XX antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
XX antigens.
XX PS
XX Claim 30; Fig 50A; 156pp; English.
XX CC
XX This invention describes a novel recombinant adenovirus comprising an HIV
XX sequence encoding an HIV antigen, where expression of the HIV antigen by
XX the recombinant adenovirus elicits an immune response directed against
XX the HIV antigen in a host upon infection of the host by the recombinant
XX adenovirus. The products of the invention have anti-HIV, virucide,
XX antibacterial, antiparasitic, protozoacide, cytostatic and
XX immunomodulatory activity. The recombinant adenoviruses are useful as
XX vaccines for eliciting immune response or conferring protection against
XX infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B,
XX C, D or E or tumour antigens. The recombinant adenoviruses are also
XX useful as genetic vaccines against pathogenic bacteria, parasites or
XX protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing
XX the immunogenicity of the HIV antigens. This sequence represents an HIV-1
XX strain BH10 antigen construct described in the disclosure of the
XX invention.
XX SQ
XX Sequence 1308 BP; 473 A; 236 C; 326 G; 273 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 129; DB 9; Length 1308;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-30;
XX Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTATTCAATAGTAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTCGTGACTTTCT 60
Db 1177 TTATTCAATAGTAGTAGGAGGCTTGGTAGGTTAAGAAATAGTTTTCGTGACTTTCT 1236
QY 61 GTAGTGAATAGTAGGAGGAGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 120
Db 1237 GTAGTGAATAGTAGGAGGAGATATTCACCATATTCGTTTCAGACCCACCTCCCAATC 1296
QY 121 CCGAGGGGA 129
Db 1297 CCGAGGGGA 1305
RESULT 10
ADB6287
ID ADD66287 standard; DNA; 1308 BP.

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XX AC ADD66287;
XX DT 15-JAN-2004 (first entry)
XX DE HIV p17/24 membrane form DNA.
XX KW virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;
XX KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
XX KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;
XX KW HIV infection; ds; gene.
XX OS Human immunodeficiency virus.
XX PN US2003138459-A1.
XX PD 24-JUL-2003.
XX PF 17-MAR-2003; 2003US-00286332.
XX PR 02-JUN-2000; 2000US-00585599.
XX PR 04-JUN-2001; 2001WO-US018238.
XX PR 01-NOV-2001; 2001US-00003035.
XX PA (WANG/) WANG D.
XX PI Wang D;
XX DR WPI; 2003-851718/79.
XX DR P-PSDB; ADD66290.
XX CC Enhancing the immunity of a host to infection of a first and second
XX PT pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or
XX PT HIV infections comprises administering to the host a first and a second
XX PT recombinant adenovirus.
XX PS Example; SEQ ID NO 36; 185pp; English.
XX CC The invention relates to a method of enhancing the immunity of a host to
XX CC infection of a first and second pathogenic virus comprising administering
XX CC to the host a first and a second recombinant adenovirus. The method is
XX CC useful for enhancing immunity of the host to infections, e.g. influenza,
XX CC Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes
XX CC simplex or human papilloma virus or HIV infections. The present sequence
XX CC is used in the exemplification of the invention.
XX SQ Sequence 1308 BP; 473 A; 236 C; 326 G; 273 T; 0 U; 0 Other;

Query Match 100.0%; Score 129; DB 9; Length 1308;
Best Local Similarity 100.0%; Pred. No. 1.9e-30;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTCATATGATAGTAGGAGGCTTGTTAGGTTTAAGATAGTTTTCGTGACTTTCT 60
DB 1177 TTATTCATATGATAGTAGGAGGCTTGTTAGGTTTAAGATAGTTTTCGTGACTTTCT 1236
QY 61 GTAGTGAATAGTAGGAGGATATTCACATATGTTTCAGACCCACCTCCCAATC 120
DB 1237 GTAGTGAATAGTAGGAGGATATTCACATATGTTTCAGACCCACCTCCCAATC 1296
QY 121 CCGAGGGGA 129
DB 1297 CCGAGGGGA 1305

RESULT 11
AAN90531
ID AAN90531 standard; DNA; 2237 BP.
XX AC AAN90531;
XX DT 25-MAR-2003 (revised)
XX DT 22-AUG-1990 (first entry)

XX DE ADD66287;
XX KW HIV; fusion protein; gag; env; AIDS; vaccine; ss.
XX OS Human T-cell lymphotropic virus III.
XX PN JP01179687-A.
XX PD 17-JUL-1989.
XX PF 30-DEC-1987; 87JP-00336292.
XX PR 30-DEC-1987; 87JP-00336292.
XX PA (KAGA ) KAGAKU OYOBI KESSEI RYOHO.
XX DR WPI; 1989-245894/34.
XX DR P-PSDB; AAP95781.
XX CC Fusion protein of hiv gag-env - effective for an aids antibody assay
XX PT reagent or vaccine - obtd. by expressing fused gene contg. fragment of
XX PT coding from human immune virus gag gene.
XX PS Claim; Page ?; 12pp; Japanese.
XX CC Fusion protein gene comprises the 0.9kbp gene fragment from PvuII site to
XX CC BglII site of HTLV-III gag gene, and 1.2kbp gene fragment from BglII site
XX CC to Xho I site of HTLV-III env gene. The HIV gag-env protein has the
XX CC antigenicity of the gag and env proteins. It contains all the peptide
XX CC domains of gag-p24 and env-gp41 that are esp. important antigens in a
XX CC vaccine. The eukaryotic expression cell is pref. Saccharomyces
XX CC cerevisiae. (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 2237 BP; 758 A; 396 C; 597 G; 486 T; 0 U; 0 Other;

Query Match 100.0%; Score 129; DB 1; Length 2237;
Best Local Similarity 100.0%; Pred. No. 2.2e-30;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTCATATGATAGTAGGAGGCTTGTTAGGTTTAAGATAGTTTTCGTGACTTTCT 60
DB 1609 TTATTCATATGATAGTAGGAGGCTTGTTAGGTTTAAGATAGTTTTCGTGACTTTCT 1668
QY 61 GTAGTGAATAGTAGGAGGATATTCACATATGTTTCAGACCCACCTCCCAATC 120
DB 1669 GTAGTGAATAGTAGGAGGATATTCACATATGTTTCAGACCCACCTCCCAATC 1728
QY 121 CCGAGGGGA 129
DB 1729 CCGAGGGGA 1737

RESULT 12
ADB87745
ID ADB87745 standard; DNA; 2280 BP.
XX AC ADB87745;
XX DT 04-DEC-2003 (first entry)
XX DE HIV-1 strain BH10 EnvmdeltaCdeltaT construct DNA SEQ ID 16.
XX KW adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
XX KW antiparasitic; protozoacide; cytosatic; immunomodulatory; vaccine;
XX KW pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
XX OS Synthetic.
XX OS Human immunodeficiency virus 1.
XX PN US2002155127-A1.
XX PD 24-OCT-2002.

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XX PF 01-NOV-2001; 2001US-00003035.
XX PR 02-JUN-2000; 2000US-00585599.
XX PR 04-JUN-2001; 2001WO-US018238.
XX PA (WANG/) WANG D.
XX PI Wang D;
XX PI WPI; 2003-182621/18.
XX DR
XX PT New recombinant adenoviruses, useful as vaccines for eliciting immune
XX PT response or conferring protection against infection of a pathogenic
XX PT antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
XX PT antigens.
XX PS Claim 12; Fig 40; 156pp; English.
XX CC This invention describes a novel recombinant adenovirus comprising an HIV
XX CC sequence encoding an HIV antigen, where expression of the HIV antigen by
XX CC the recombinant adenovirus elicits an immune response directed against
XX CC the HIV antigen in a host upon infection of the host by the recombinant
XX CC adenovirus. The products of the invention have anti-HIV, virucide,
XX CC antibacterial, antiparasitic, protozoacide, cytostatic and
XX CC immunomodulatory activity. The recombinant adenoviruses are useful as
XX CC vaccines for eliciting immune response or conferring protection against
XX CC infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B,
XX CC C, D or E or tumour antigens. The recombinant adenoviruses are also
XX CC useful as genetic vaccines against pathogenic bacteria, parasites or
XX CC protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing
XX CC the immunogenicity of the HIV antigens. This sequence represents an HIV-1
XX CC strain BH10 antigen construct described in the disclosure of the
XX CC invention.
XX SQ Sequence 2280 BP; 802 A; 386 C; 534 G; 558 T; 0 U; 0 Other;

Query Match 100.0%; Score 129; DB 9; Length 2280;
Best Local Similarity 100.0%; Pred. No. 2.2e-30;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTCATATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 60
Db 2056 TTATTCATATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTGTGCTACTTTCT 2115
QY 61 GTAGTGAATAGAGTTAGGAGGATATTCACCATTCGTTTCAGACCCACCTCCCAATC 120
Db 2116 GTAGTGAATAGAGTTAGGAGGATATTCACCATTCGTTTCAGACCCACCTCCCAATC 2175
QY 121 CCGAGGGGA 129
Db 2176 CCGAGGGGA 2184

RESULT 14
AAN80949
ID AAN80949 standard; DNA; 2553 BP.
XX AC AAN80949;
XX XX
XX DT 24-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 15-NOV-1990 (first entry)
XX XX
XX DE HIV protein HT6.
XX XX
XX KW HIV; HT6; gp160; envelope protein; RF; AIDS; ss.
XX OS Human immunodeficiency virus; variant RF.
XX XX
XX PN EP272858-A.
XX PD 29-JUN-1988.
XX XX
XX PF 14-DEC-1987; 87EP-00310967.
XX XX
XX PR 15-DEC-1986; 86US-00941111.
XX PR 31-AUG-1987; 87US-00091481.
XX XX

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PA (REPK ) REPLIGEN CORP.
XX
XX Rusche J, Lynn D, Carson H, Putney S, Jellis CL;
XX
XX WPI; 1988-176944/26.
DR P-PSDB; AAP80967.
XX
XX Prodn. of recombinant HIV envelope proteins in insect cells - useful as
PT vaccine against AIDS and for diagnosis and therapy.
XX
XX Disclosure; Page ?; 4pp; English.
XX
XX The sequence is the result of cloning a hybrid envelope gene from HIV
CC variants BH10 and RF. A central portion of the RF gene was used, the rest
CC being from te distantly related variant BH10. The resulting clone, pACHT6
CC produces a hybrid gp 160 envelope protein with novel immunological and
CC antigenic characteristics. It may be used to as a vaccine and for
CC diagnosis and therapy of AIDS. See also AAN80948. (Updated on 25-MAR-2003
CC to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 2553 BP; 887 A; 430 C; 613 G; 623 T; 0 U; 0 Other;
Query Match 100.0%; Score 129; DB 1; Length 2553;
Best Local Similarity 100.0%; Pred. No. 2.2e-30;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTCGCTGCTACTTTCT 60
DB 2035 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTCGCTGCTACTTTCT 2094
QY 61 GTAGTGAATAGAGTTAGGAGGAGATATTCCACATTATCGTTTCAGACCCACCTCCCAATC 120
DB 2095 GTAGTGAATAGAGTTAGGAGGAGATATTCCACATTATCGTTTCAGACCCACCTCCCAATC 2154
QY 121 CCGAGGGGA 129
DB 2155 CCGAGGGGA 2163
RESULT 15
ADB87753
ID ADB87753 standard; DNA; 2583 BP.
XX
XX ADB87753;
XX
XX 04-DEC-2003 (first entry)
XX
XX HIV-1 BH10 construct EM/Em SEQ ID 24.
XX
XX adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
XX antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;
XX pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
XX
XX Human immunodeficiency virus 1.
XX
XX US2002155127-A1.
XX
XX 24-OCT-2002.
XX
XX 01-NOV-2001; 2001US-00003035.
XX
XX 02-JUN-2000; 2000US-00585599.
XX
XX 04-JUN-2001; 2001WO-US018238.
XX
XX (WANG/) WANG D.
XX
XX Wang D;
XX
XX WPI; 2003-182621/18.
XX
XX New recombinant adenoviruses, useful as vaccines for eliciting immune
PT response or conferring protection against infection of a pathogenic
PT antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor

```

```

PT antigens.
XX
XX Claim 12; Fig 47; 156pp; English.
XX
XX This invention describes a novel recombinant adenovirus comprising an HIV
CC sequence encoding an HIV antigen, where expression of the HIV antigen by
CC the recombinant adenovirus elicits an immune response directed against
CC the HIV antigen in a host upon infection of the host by the recombinant
CC adenovirus. The products of the invention have anti-HIV, virucide,
CC antibacterial, antiparasitic, protozoacide, cytostatic and
CC immunomodulatory activity. The recombinant adenoviruses are useful as
CC vaccines for eliciting immune response or conferring protection against
CC infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B,
CC C, D or E or tumour antigens. The recombinant adenoviruses are also
CC useful as genetic vaccines against pathogenic bacteria, parasites or
CC protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing
CC the immunogenicity of the HIV antigens. This sequence represents an HIV-1
CC strain BH10 antigen construct described in the disclosure of the
XX invention.
XX
XX SQ Sequence 2583 BP; 892 A; 441 C; 621 G; 629 T; 0 U; 0 Other;
Query Match 100.0%; Score 129; DB 9; Length 2583;
Best Local Similarity 100.0%; Pred. No. 2.2e-30;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTCGCTGCTACTTTCT 60
DB 2062 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTCGCTGCTACTTTCT 2121
QY 61 GTAGTGAATAGAGTTAGGAGGAGATATTCCACATTATCGTTTCAGACCCACCTCCCAATC 120
DB 2122 GTAGTGAATAGAGTTAGGAGGAGATATTCCACATTATCGTTTCAGACCCACCTCCCAATC 2181
QY 121 CCGAGGGGA 129
DB 2182 CCGAGGGGA 2190
Search completed: March 11, 2004, 20:49:42
Job time : 306.156 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 20:30:23 ; Search time 45.4128 Seconds
(without alignments)
1099.812 Million cell updates/sec

Title: US-10-003-035-74
Perfect score: 90
Sequence: 1 atgagagtgaagagaata.....tggtgatgattctagtgt 90

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
 - 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
 - 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
 - 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
 - 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
 - 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	105	1	US-08-029-402-14
2	90	100.0	2020	2	US-08-417-210A-135
3	90	100.0	2020	4	US-09-136-159A-135
4	90	100.0	2028	2	US-08-417-210A-138
5	90	100.0	2028	4	US-09-136-159A-138
6	90	100.0	2060	2	US-08-417-210A-141
7	90	100.0	2060	4	US-09-136-159A-141
8	90	100.0	2571	2	US-07-916-098A-1
9	90	100.0	2694	1	US-08-147-890-1
10	90	100.0	2696	4	US-09-325-131B-1
11	90	100.0	2730	3	US-08-728-122-1
12	90	100.0	2945	6	5462872-1
13	90	100.0	3084	1	US-08-147-890-2
14	90	100.0	3563	3	US-08-463-210-6
15	90	100.0	3563	4	US-08-463-028-6
16	90	100.0	3807	2	US-08-417-210A-78
17	90	100.0	3807	4	US-09-136-159A-78
18	90	100.0	8932	3	US-09-124-900-1
19	90	100.0	8933	3	US-08-463-210-4
20	90	100.0	8933	3	US-09-620-958A-3
21	90	100.0	8933	3	US-09-620-958A-4
22	90	100.0	8933	3	US-09-620-958A-9
23	90	100.0	8933	4	US-08-463-028-4
24	90	100.0	9719	4	US-09-700-304-1
25	88.4	98.2	2184	4	US-09-337-387-4
26	86.8	96.4	2531	3	US-07-956-483-18
27	86.8	96.4	2644	3	US-08-472-240A-9

28	85.2	94.7	9709	2	US-08-188-583-5	Sequence 5, Appli
29	85.2	94.7	9709	3	US-08-388-353-1	Sequence 1, Appli
30	85.2	94.7	9709	3	US-08-488-551B-1	Sequence 1, Appli
31	85.2	94.7	9709	4	US-09-309-572-15	Sequence 15, Appl
32	85.2	94.7	12479	4	US-09-718-096-15	Sequence 15, Appl
33	85.2	94.7	12479	4	US-09-318-138-13	Sequence 13, Appl
34	85.2	94.7	12494	3	US-08-935-312-13	Sequence 13, Appl
35	85.2	94.7	12494	3	US-08-848-760B-33	Sequence 33, Appl
36	85.2	94.7	15581	3	US-08-646-538-35	Sequence 35, Appl
37	85.2	94.7	15581	3	US-09-503-222-35	Sequence 35, Appl
38	81.2	90.2	7399	2	US-08-418-848A-9	Sequence 9, Appli
39	66.8	74.2	7616	3	US-08-815-809-6	Sequence 6, Appli
40	66.8	74.2	7797	2	US-08-816-155B-7	Sequence 7, Appli
41	66.8	74.2	7797	3	US-09-079-587-7	Sequence 7, Appli
42	66.8	74.2	10962	2	US-08-816-155B-6	Sequence 6, Appli
43	66.8	74.2	10962	3	US-09-079-587-6	Sequence 6, Appli
44	66.8	74.2	19877	2	US-08-816-155B-8	Sequence 8, Appli
45	66.8	74.2	19877	3	US-09-079-587-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-029-402-14
; Sequence 14, Application US/08029402
; Patent No. 5516657
; GENERAL INFORMATION:
; APPLICANT: Murphy, Cheryl I.
; TITLE OF INVENTION: Baculovirus Vectors For Expression of
; TITLE OF INVENTION: Secretory and Membrane-Bound Proteins
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,402
; FILING DATE: 19930305
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0614.0860001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..105
US-08-029-402-14

Query Match 100.0%; Score 90; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.2e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGTGCAGGAGAGAAATATCAGCACTGTGGAGATCGGGTGGAGATGGGCAACCATG 60

Db 10 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 69
Qy 61 CTCCTTGGGATGTTGATGACTGTAGTGCT 90
Db 70 CTCCTTGGGATGTTGATGACTGTAGTGCT 99

RESULT 2

US-08-417-210A-135
; Sequence 135, Application US/08417210A
; Patent No. 5863542
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: 148
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2690
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-840-3333
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2020 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-417-210A-135

Query Match 100.0%; Score 90; DB 2; Length 2020;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 60
Db 297 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 356
Qy 61 CTCCTTGGGATGTTGATGACTGTAGTGCT 90
Db 357 CTCCTTGGGATGTTGATGACTGTAGTGCT 386

RESULT 3

US-09-136-159A-135
; Sequence 135, Application US/09136159A
; Patent No. 6596279
; GENERAL INFORMATION:
; APPLICANT: Virogenetics Corporation
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/09/136.159A

; CURRENT FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: US 08/417,210
; PRIOR FILING DATE: 1995-04-05
; PRIOR APPLICATION NUMBER: US 08/223,842
; PRIOR FILING DATE: 1994-04-06
; PRIOR APPLICATION NUMBER: US 07/897,382
; PRIOR FILING DATE: 1992-06-11
; PRIOR APPLICATION NUMBER: US 07/715,921
; PRIOR FILING DATE: 1991-06-14
; PRIOR APPLICATION NUMBER: US 08/105,483
; PRIOR FILING DATE: 1993-08-12
; PRIOR APPLICATION NUMBER: US 07/847,951
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: US 07/713,967
; PRIOR FILING DATE: 1991-06-11
; PRIOR APPLICATION NUMBER: US 07/666,056
; PRIOR FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 2020
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of the H6-promoted HIV1 gp120 + TM (with ELDKWA ep:
; OTHER INFORMATION: opes) gene between C5 flanking arms, coding strand
; US-09-136-159A-135

Query Match 100.0%; Score 90; DB 4; Length 2020;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 60
Db 297 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATTG 356
Qy 61 CTCCTTGGGATGTTGATGACTGTAGTGCT 90
Db 357 CTCCTTGGGATGTTGATGACTGTAGTGCT 386

RESULT 4

US-08-417-210A-138
; Sequence 138, Application US/08417210A
; Patent No. 5863542
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,210A
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2690
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-840-3333

; INFORMATION FOR SEQ ID NO: 138:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2028 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-417-210A-138

Query Match 100.0%; Score 90; DB 2; Length 2028;

Best Local Similarity 100.0%; Pred. No. 5.4e-21;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGAGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60

Db 297 ATGAGAGTGAAGAGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 356

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

Db 357 CTCCTTGGGATGTTGATGATCTGTAGTGCT 386

RESULT 5

US-09-136-159A-138

; Sequence 138, Application US/09136159A

; Patent No. 6596279

; GENERAL INFORMATION:

; APPLICANT: Virogenetics Corporation

; APPLICANT: Paolletti, Enzo

; APPLICANT: Tartaglia, James

; APPLICANT: Cox, William I

; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus

; FILE REFERENCE: 454310-2690.1

; CURRENT APPLICATION NUMBER: US/09/136, 159A

; CURRENT FILING DATE: 1998-08-14

; PRIOR APPLICATION NUMBER: US 08/417,210

; PRIOR FILING DATE: 1995-04-05

; PRIOR APPLICATION NUMBER: US 08/223,842

; PRIOR FILING DATE: 1994-04-06

; PRIOR APPLICATION NUMBER: US 07/897,382

; PRIOR FILING DATE: 1992-06-11

; PRIOR APPLICATION NUMBER: US 07/715,921

; PRIOR FILING DATE: 1991-06-14

; PRIOR APPLICATION NUMBER: US 08/105,483

; PRIOR FILING DATE: 1993-08-12

; PRIOR APPLICATION NUMBER: US 07/847,951

; PRIOR FILING DATE: 1992-03-06

; PRIOR APPLICATION NUMBER: US 07/713,967

; PRIOR FILING DATE: 1991-06-11

; PRIOR APPLICATION NUMBER: US 07/666,056

; PRIOR FILING DATE: 1991-03-07

; NUMBER OF SEQ ID NOS: 149

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 138

; LENGTH: 2028

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Nucleotide sequence of H6-promoted HIV1 gp120 + TM (with ELDKWA

; OTHER INFORMATION: pitopes) gene between 14L flanking arms, coding strand.

US-09-136-159A-138

Query Match

Best Local Similarity 100.0%; Score 90; DB 4; Length 2028;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGAGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60

Db 297 ATGAGAGTGAAGAGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 356

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

Db 357 CTCCTTGGGATGTTGATGATCTGTAGTGCT 386

RESULT 6

US-08-417-210A-141

; Sequence 141, Application US/08417210A

; Patent No. 5863542

; GENERAL INFORMATION:

; APPLICANT: PAOLETTI, ENZO

; APPLICANT: TARTAGLIA, JAMES

; APPLICANT: COX, WILLIAM I.

; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS

; NUMBER OF SEQUENCES: 148

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.

; STREET: 530 FIFTH AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/417,210A

; FILING DATE: 05-APR-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: KOWALSKI, THOMAS J.

; REGISTRATION NUMBER: 32,147

; REFERENCE/DOCKET NUMBER: 454310-2690

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-840-3333

; INFORMATION FOR SEQ ID NO: 141:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2060 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-417-210A-141

Query Match 100.0%; Score 90; DB 2; Length 2060;

Best Local Similarity 100.0%; Pred. No. 5.4e-21;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGAGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60

Db 297 ATGAGAGTGAAGAGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCCACCATG 356

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

Db 357 CTCCTTGGGATGTTGATGATCTGTAGTGCT 386

RESULT 7

US-09-136-159A-141

; Sequence 141, Application US/09136159A

; Patent No. 6596279

; GENERAL INFORMATION:

; APPLICANT: Virogenetics Corporation

; APPLICANT: Paolletti, Enzo

; APPLICANT: Tartaglia, James

; APPLICANT: Cox, William I

; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus

; FILE REFERENCE: 454310-2690.1

; CURRENT APPLICATION NUMBER: US/09/136,159A

; CURRENT FILING DATE: 1998-08-14

; PRIOR APPLICATION NUMBER: US 08/417,210

; PRIOR FILING DATE: 1995-04-05

; PRIOR APPLICATION NUMBER: US 08/223,842

; PRIOR FILING DATE: 1994-04-06


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; PRIOR APPLICATION NUMBER: US 07/897,382
; PRIOR FILING DATE: 1992-06-11
; PRIOR APPLICATION NUMBER: US 07/715,921
; PRIOR FILING DATE: 1991-06-14
; PRIOR APPLICATION NUMBER: US 08/105,483
; PRIOR FILING DATE: 1993-08-12
; PRIOR APPLICATION NUMBER: US 07/847,951
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: US 07/713,967
; PRIOR FILING DATE: 1991-06-11
; PRIOR APPLICATION NUMBER: US 07/666,056
; PRIOR FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 141
; LENGTH: 2060
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: H6-promoted HIV1 gp120 + TM (with ELDKWA epitopes) gene between A
; OTHER INFORMATION: 24R and K1L flanking arms, coding sequence
US-09-136-159A-141

Query Match          100.0%; Score 90; DB 4; Length 2060;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
DB 297 ATGAGAGTGAAGGAGAAATATCAGCACTGTGGAGATGGGGTGGAGATGGGGCCACCATG 356

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 357 CTCCTTGGGATGTTGATGATCTGTAGTGCT 386

RESULT 8
US-07-916-098A-1
; Sequence 1, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916.098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
```

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; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 25,949
; REFERENCE/DOCKET NUMBER: 52,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..87
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 88..2568
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1533..1534
; OTHER INFORMATION: /note= "gp120/gp41 cleavage site"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2568
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "pre-HIV gp160"
US-07-916-098A-1

Query Match          100.0%; Score 90; DB 2; Length 2571;
Best Local Similarity 100.0%; Pred. No. 5.8e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60
DB 1 ATGAGAGTGAAGGAGAAATATCAGCACTGTGGAGATGGGGTGGAGATGGGGCCACCATG 60

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

RESULT 9
US-08-147-890-1
; Sequence 1, Application US/08147890
; Patent No. 5714316
; GENERAL INFORMATION:
; APPLICANT: Weiner, David
; APPLICANT: Williams, William
; APPLICANT: Levy, David N.
; TITLE OF INVENTION: Chimeric Envelope Proteins for Viral
; TITLE OF INVENTION: Targeting
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,890
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/719,537
; FILING DATE: 21-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST15AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2694 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-147-890-1

Query Match      100.0%; Score 90; DB 1; Length 2694;
Best Local Similarity 100.0%; Pred. No. 5.9e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGGAGATGGGGCACCATG 60
DB 271 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGGAGATGGGGCACCATG 330

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 331 CTCCTTGGGATGTTGATGATCTGTAGTGCT 360

RESULT 10
US-09-325-131B-1
; Sequence 1, Application US/09325131B
; Patent No. 6492104
; GENERAL INFORMATION:
; APPLICANT: CLOYD, MILES W.
; APPLICANT: RAMSEY, KEITH
; TITLE OF INVENTION: EIA TEST USING NONDENATURED HIV ANTIGEN FOR EARLY
; TITLE OF INVENTION: DETECTION OF HIV INFECTION
; FILE REFERENCE: UTSG:234
; CURRENT APPLICATION NUMBER: US/09/325,131B
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 08/728,122
; PRIOR FILING DATE: 1996-10-09
; PRIOR APPLICATION NUMBER: 08/143,168
; PRIOR FILING DATE: 1993-10-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 2696
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-325-131B-1

Query Match      100.0%; Score 90; DB 4; Length 2696;
Best Local Similarity 100.0%; Pred. No. 5.9e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGGAGATGGGGCACCATG 60
DB 440 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGGAGATGGGGCACCATG 499

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 500 CTCCTTGGGATGTTGATGATCTGTAGTGCT 529

RESULT 11
US-08-728-122-1
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; Sequence 1, Application US/08728122
; Patent No. 6074646
; GENERAL INFORMATION:
; APPLICANT: CLOYD, MILES W.
; APPLICANT: RAMSEY, KEITH M.
; TITLE OF INVENTION: A New EIA Test Using No. 6074646-Denatured
; TITLE OF INVENTION: HIV Antigen for Early Detection of
; TITLE OF INVENTION: HIV Infection
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
; STREET: 816 Congress Avenue, Suite 1900
; CITY: Austin
; STATE: Texas
; COUNTRY: USA
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,122
; FILING DATE: 09-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: 43424.0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 499-6200
; TELEFAX: (512) 499-6290
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2730 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-728-122-1

Query Match      100.0%; Score 90; DB 3; Length 2730;
Best Local Similarity 100.0%; Pred. No. 5.9e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGGAGATGGGGCACCATG 60
DB 470 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGGAGATGGGGCACCATG 529

QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 530 CTCCTTGGGATGTTGATGATCTGTAGTGCT 559

RESULT 12
5462872-1
; Patent No. 5462872
; APPLICANT: Jonak, Zdenka L.; Debouck, Christine; Clark, Robert
; Trulli, Stephen
; TITLE OF INVENTION: HUMAN LYMPHOID CELLS EXPRESSING HUMAN
; IMMUNODEFICIENCY VIRUS ENVELOPE PROTEIN GP160
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,128
; FILING DATE: 08-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 906,613
; FILING DATE: 30-JUN-1992
; APPLICATION NUMBER: 587,011
; FILING DATE: 24-SEP-1990
; SEQ ID NO: 1
; LENGTH: 2945
5462872-1
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Query Match 100.0%; Score 90; DB 6; Length 2945;
Best Local Similarity 100.0%; Pred. No. 6e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGACCTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60
DB 268 ATGAGAGTGAAGGAGAAATATCAGACCTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 327
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 328 CTCCTTGGGATGTTGATGATCTGTAGTGCT 357

RESULT 13

US-08-147-890-2
; Sequence 2, Application US/08147890
; Patent No. 5714316
; GENERAL INFORMATION:
; APPLICANT: Weiner, David
; APPLICANT: Williams, William
; APPLICANT: Levy, David N.
; TITLE OF INVENTION: Chimeric Envelope Proteins for Viral
; TITLE OF INVENTION: Targeting
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,890
; FILING DATE:
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/718,537
; FILING DATE: 21-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST15AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3084 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-147-890-2

Query Match 100.0%; Score 90; DB 1; Length 3084;
Best Local Similarity 100.0%; Pred. No. 6.1e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGACCTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60
DB 271 ATGAGAGTGAAGGAGAAATATCAGACCTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 330
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 331 CTCCTTGGGATGTTGATGATCTGTAGTGCT 360

RESULT 14

US-08-463-028-6
; Sequence 6, Application US/08463028
; Patent No. 6610476

US-08-463-210-6
; Sequence 6, Application US/08463210
; Patent No. 6001977
; GENERAL INFORMATION:
; APPLICANT: CHANG, Nancy T.
; APPLICANT: GALLO, Robert C.
; APPLICANT: WONG-STAAAL, Floissie
; TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154-0053

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,210
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 436

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/693,866
; FILING DATE: 23-JAN-1985
; APPLICATION NUMBER: US 06/659,339
; FILING DATE: 10-OCT-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Serunian, Leslie A.

REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4193US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 758-4800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

LENGTH: 3563 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: HTLV-III
; FEATURE:

NAME/KEY: misc feature
; LOCATION: 1..3563
; OTHER INFORMATION: /standard name= "Clone BH8"
; OTHER INFORMATION: /note= "Corresponds to nucleotide positions 5580
; OTHER INFORMATION: to 9154 in figure 3 of US 06/693,866"

US-08-463-210-6
Query Match 100.0%; Score 90; DB 3; Length 3563;
Best Local Similarity 100.0%; Pred. No. 6.4e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGTGAAGGAGAAATATCAGACCTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60
DB 226 ATGAGAGTGAAGGAGAAATATCAGACCTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 285
QY 61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
DB 286 CTCCTTGGGATGTTGATGATCTGTAGTGCT 315

GENERAL INFORMATION:
APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, Robert C.
APPLICANT: WONG-STAL, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,028
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3563 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HTLV-III
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..3563
OTHER INFORMATION: /standard name= "Clone BH8"
OTHER INFORMATION: /note= "Corresponds to nucleotide positions 5580
OTHER INFORMATION: to 9154 in figure 3 of US 06/693,866"

US-08-463-028-6
Query Match 100.0%; Score 90; DB 4; Length 3563;
Best Local Similarity 100.0%; Pred. No. 6.4e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG	60
Db	226	ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG	285
QY	61	CTCCTTGGGATGTTGATGATCTGTAGTGCT	90
Db	286	CTCCTTGGGATGTTGATGATCTGTAGTGCT	315

Search completed: March 11, 2004, 23:12:15
Job time : 47.4128 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 19:37:35 ; Search time 2481.77 Seconds
(without alignments)
1552.207 Million cell updates/sec

Title: US-10-003-035-75

Perfect score: 129

Sequence: 1 ttattcataatgatagtagg.....acctccaatccgagggga 129

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_liv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	ID	Description
1	79	61.2	145	9 AB036493	AB036493 AB036493
2	70	54.3	232	29 HSMC01D05	X88515 H.sapiens D
3	37.4	29.0	110	29 CG788669	CG788669 ZMMBB024
4	35.8	27.8	816	29 CG453676	CG453676 OGVGU637H

C	5	35.8	27.8	851	29	CG453685	OGVU637TV
C	6	35.8	27.8	936	29	CG416525	ZMMBBc002
C	7	34.2	26.5	270	29	CG019434	CG019434 ZUARN74TH
C	8	34.2	26.5	782	28	CC167485	CC167485 IK30c12.9
C	9	34.2	26.5	794	28	BH332797	BH332797 CH230-591
C	10	34.2	26.5	805	29	CC986340	CC986340 ZUAPW74TH
C	11	34.2	26.5	807	29	CC670625	CC670625 QWBT24TV
C	12	34.2	26.5	935	29	CG464137	CG464137 ZUARN35TV
C	13	33.4	25.9	513	13	BQ098469	BQ098469 ph18c07.Y
C	14	33.4	25.9	535	13	BQ099257	BQ099257 ph28c05.Y
C	15	33.4	25.9	536	13	BQ099653	BQ099653 ph33a09.Y
C	16	33.4	25.9	664	13	BQ26142	BQ26142 ph89h12.Y
C	17	33.4	25.9	711	29	CG603354	CG603354 QGRBT05TV
C	18	33.2	25.7	486	10	B8919849	B8919849 EST423618
C	19	33.2	25.7	490	10	B8919553	B8919553 EST423322
C	20	33.2	25.7	603	28	BH760799	BH760799 BMBAC317B
C	21	33.2	25.7	696	12	B1435067	B1435067 EST537828
C	22	33.2	25.7	704	13	BQ516427	BQ516427 EST623842
C	23	33.2	25.7	722	14	CK261624	CK261624 EST707702
C	24	33.2	25.7	747	12	B1433251	B1433251 EST536012
C	25	33.2	25.7	747	13	BQ516428	BQ516428 EST623843
C	26	33.2	25.7	756	14	CK261623	CK261623 EST707701
C	27	33.2	25.7	951	14	CK263442	CK263442 EST709520
C	28	33	25.6	513	13	BQ538010	BQ538010 pz08f12.Y
C	29	33	25.6	799	29	CC986983	CC986983 ZUABE85TH
C	30	32.6	25.3	509	29	CG228280	CG228280 QGWHN17TH
C	31	32.6	25.3	521	29	CG015492	CG015492 ZUABX13TH
C	32	32.6	25.3	722	29	CC829271	CC829271 ZMMBB017
C	33	32.6	25.3	860	29	CC731889	CC731889 OGULX43TV
C	34	32.6	25.3	868	29	CC667508	CC667508 OGUKC77TH
C	35	32.4	25.1	416	12	BJ368213	BJ368213 BJ368213
C	36	32.4	25.1	495	12	BJ411212	BJ411212 BJ411212
C	37	32.4	25.1	550	12	BJ370269	BJ370269 BJ370269
C	38	32.4	25.1	597	12	BJ370029	BJ370029 BJ370029
C	39	32.4	25.1	602	12	BJ366287	BJ366287 BJ366287
C	40	32.4	25.1	605	12	BJ397521	BJ397521 BJ397521
C	41	32.4	25.1	611	12	BJ368768	BJ368768 BJ368768
C	42	32.4	25.1	615	12	BJ425039	BJ425039 BJ425039
C	43	32.4	25.1	627	12	BJ424063	BJ424063 BJ424063
C	44	32.4	25.1	628	12	BJ367814	BJ367814 BJ367814
C	45	32.4	25.1	639	12	BJ425027	BJ425027 BJ425027

ALIGNMENTS

RESULT 1	AB036493	145 bp	mRNA	linear	EST 22-AUG-2000
LOCUS	AB036493	Mus musculus Cj7 brain, liver, kidney, lung, heart Mus			
DEFINITION	AB036493	musculus CDNA clone 15-5, mRNA sequence.			
ACCESSION	AB036493	GI:6854226			
VERSION	AB036493.1	EST.			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 145)				
AUTHORS	Wang, Y. B., Saigon, K., Osaka, H., Yamanishi, T., Suh, J. G., Kiyosawa, H., Sakai, Y., Wakana, S. and Wada, K.				
TITLE	YAC/BAC-Based physical and transcript mapping around the gracile axonal dystrophy (gad) locus identifies uchl1, pmx2b, atp3a2, and hip2 genes				
JOURNAL	Genomics 66 (3), 333-336 (2000)				
MEDLINE	20334630				
PUBMED	10873389				
COMMENT	Contact: Keiji Wada Department of Degenerative Neurological Diseases National Institute of Neuroscience, NCNP 4-1-1, Ogawahigashi, Kodaira, Tokyo 187-8502, Japan Email: wada@ncnp.go.jp RT-PCR primer based on the sequence that isolated from mouse BAC				

clones (414D20, 220F19, Research Genetics) using exon trapping method.

FEATURES

source
Location/Qualifiers
1..145
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129/Sv"
/db_xref="taxon:10090"
/map="5"
/clones="15-5"
/sex="male"
/tissue_type="brain, liver, kidney, lung, heart"
/cell_lines="CJ7 embryonic stem cell line"
/dev_stage="adult"
/clone_lib="Mus musculus CJ7 brain, liver, kidney, lung, heart"

ORIGIN

Query Match 61.2%; Score 79; DB 9; Length 145;
Best Local Similarity 88.5%; Pred. No. 3.2e-13;
Matches 100; Conservative 0; Mismatches 5; Indels 8; Gaps 1;
Qy 1 TTATTCATATGATAGTAGGAGGCTTGCTAGGTT-----TAAGTAATAGTTTTCGTCG 52
Db 33 TTATTCATATGATAGTAGGAGGCTTGCTAGGTTGTAAGTAATACATGTAATTTTTCGTCG 92
Qy 53 TACTTTCGTAGTGAATAGAGTTAGGAGGATATTCACCATATTCGTTTCAG 105
Db 93 TACTTTCGTAGTGAATAGAGTTAGGAGGATATTCACCATATTCGTTTCAG 145

RESULT 2
HSMC01D05 232 bp DNA linear GSS 29-MAY-1997
LOCUS H.sapiens DNA for trapped exon (ID HMC01D05), genomic survey sequence.
X88515
VERSION X88515.1 GI:1437515
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 232)
AUTHORS Chen,H., Chrast,R., Rossier,C., Morris,M.A., Laliet,M.D. and Antonarakis,S.E.
TITLE Cloning of 559 potential exons of genes of human chromosome 21 by exon trapping
JOURNAL Genome Res. 6 (8), 747-760 (1996)
MEDLINE 97011340
PUBMED 8858350
REFERENCE 2 (bases 1 to 232)
AUTHORS Chen,H.M., Rossier,C., Chrast,R. and Antonarakis,S.E.
TITLE Cloning of trapped exons from human chromosome 21
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 232)
AUTHORS Antonarakis,S.E.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of Medical Genetics, University and Cantonal Hospital of Geneva, CMU, Rue Michel-Servet, 1211 Geneva, SWITZERLAND

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
1..232
/note="trapped exon"

ORIGIN

Query Match 54.3%; Score 70; DB 29; Length 232;
Best Local Similarity 86.4%; Pred. No. 1.7e-10;

Matches 95; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
Qy 1 TTATTCATATGATAGTAGGAGGCTTGCTAGGTT-----TTAAGTAATAGTTTTCGTCGTA 59
Db 117 TTATTCATATGATAGTAGGAGGCTTGCTAGGTTCTCANGAATAGGTCGTCGTCGTA 176
Qy 60 TGTAAGT-GAATAGAGTTAGGAGGATATTCACCATATTCGTTTCAGACC 108
Db 177 TGTAAGTATAGTAGAGTTAGGAGGATATTCACCATATTCGNTCAGACC 236

RESULT 3
CG788669 110 bp DNA linear GSS 07-NOV-2003
LOCUS ZMMBB0243B19.r ZMMBB Zea mays subsp. mays genomic clone
DEFINITION ZMMBB0243B19 3', genomic survey sequence.
ACCESSION CG788669
VERSION CG788669.1 GI:38205005
KEYWORDS GSS.
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 110)
AUTHORS Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J. and Wing,R.
TITLE Sequencing of the maize genome
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0243 row: B column: 19
Seq primer: M13r
Class: BAC ends.
Location/Qualifiers
1..110
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/mol_type="genomic DNA"
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/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBB0243B19"
/lab_host="DH10B"
/clone_lib="ZMMBBb"
/note="vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"

ORIGIN
Query Match 29.0%; Score 37.4; DB 29; Length 110;
Best Local Similarity 64.4%; Pred. No. 0.04;
Matches 56; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 4 TTCATAATGATAGTAGGAGGCTTGCTAGGTTTAAAGATAGTTTTCGTCGTA 63
Db 8 TTAATAAAATAGTTTTCATGATTTTAGGTTAAATAGGAATTTTAAAGGATTTAAAGTA 67
Qy 64 GTGATAGAGTTAGGAGGATATTC 90
Db 68 GTTAAAGTGTAGTTATGATTTT 94

FEATURES

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Location/Qualifiers
1..110
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBB0243B19"
/lab_host="DH10B"
/clone_lib="ZMMBBb"
/note="vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 29.0%; Score 37.4; DB 29; Length 110;
Best Local Similarity 64.4%; Pred. No. 0.04;
Matches 56; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 4 TTCATAATGATAGTAGGAGGCTTGCTAGGTTTAAAGATAGTTTTCGTCGTA 63
Db 8 TTAATAAAATAGTTTTCATGATTTTAGGTTAAATAGGAATTTTAAAGGATTTAAAGTA 67
Qy 64 GTGATAGAGTTAGGAGGATATTC 90
Db 68 GTTAAAGTGTAGTTATGATTTT 94

RESULT 4

CG453676 816 bp DNA linear GSS 17-SEP-2003
LOCUS

```

DEFINITION  OGVGU63TH ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMA0479K05,
              genomic survey sequence.
ACCESSION   CG453676
VERSION     CG453676.1 GI:34838676
KEYWORDS    GSS.
SOURCE      Zea mays
            Zea mays
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 816)
AUTHORS    Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
              Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
              Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
              Consortium for Maize Genomics
              Unpublished (2002)
TITLE      Other GSSs: OGVGU63TV
JOURNAL    Contact: Cathy Whitelaw
COMMENT    TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301-838-5843
              Fax: 301-838-0208
              Email: whitelaw@tigr.org
              Seq primer: TR
              Class: sheared ends.
FEATURES    Location/Qualifiers
             source
              1..816
              /organism="Zea mays"
              /mol_type="genomic DNA"
              /strain="B73"
              /db_xref="taxon:4577"
              /clone="ZMMBMA0479K05"
              /clone_lib="ZM 0.7_1.5_KB"
              /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
              methylation filtered genomic DNA library"
ORIGIN
Query Match      27.8%; Score 35.8; DB 29; Length 816;
Best Local Similarity 63.2%; Pred. No. 3.3;
Matches 55; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY  4  TTCATATGATAGTAGGAGCTGGTAGGTTAAGATAGTTTTCGTGACTTCTGTA 63
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Db  525 TTAATAAAATAGTGTATGATTTTAGGTTAAATAAGGATTTTAAAGCATTTAAGTA 584
    |||||

QY  64  GTCAATAGAGTTAGGCAGGATATCA 90
    |||||
Db  585 GTTAAAGTATTAGTCTGGATTTTA 611
    |||||

RESULT 5
CG453685/c
LOCUS      OGVGU63TV ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMA0479K05,
DEFINITION genomic survey sequence.
ACCESSION   CG453685
VERSION     CG453685.1 GI:34838685
KEYWORDS    GSS.
SOURCE      Zea mays
            Zea mays
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 851)
AUTHORS    Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
              Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
              Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
              Consortium for Maize Genomics
              Unpublished (2002)
TITLE      Other GSSs: OGVGU63TH
JOURNAL    Contact: Cathy Whitelaw
COMMENT    TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA

```

```

Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
source
  1..851
  /organism="Zea mays"
  /mol_type="genomic DNA"
  /strain="B73"
  /db_xref="taxon:4577"
  /clone="ZMMBMA0479K05"
  /clone_lib="ZM 0.7_1.5_KB"
  /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
  methylation filtered genomic DNA library"
ORIGIN
Query Match      27.8%; Score 35.8; DB 29; Length 851;
Best Local Similarity 63.2%; Pred. No. 3.3;
Matches 55; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY  4  TTCATATGATAGTAGGAGCTGGTAGGTTAAGATAGTTTTCGTGACTTCTGTA 63
    |||||
Db  705 TTAATAAAATAGTGTATGATTTTAGGTTAAATAAGGATTTTAAAGCATTTAAGTA 646
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QY  64  GTCAATAGAGTTAGGCAGGATATCA 90
    |||||
Db  645 GTTAAAGTATTAGTCTGGATTTTA 619
    |||||

RESULT 6
CG416525
LOCUS      ZMMBBC0024C16f ZMMBBC (ECORI) Zea mays subsp. mays genomic clone
DEFINITION ZMMBBC0024C16 5', genomic survey sequence.
ACCESSION   CG416525
VERSION     CG416525.1 GI:34561370
KEYWORDS    GSS.
SOURCE      Zea mays subsp. mays (maize)
            Zea mays subsp. mays
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 936)
AUTHORS    Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
              Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
              Sequencing of the maize genome at PGIR (2003c)
              Unpublished (2003)
              Contact: Bharti,A.K.
              Dr.Joachim Messing's lab
              The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
              University
              190 Frelinghuysen Road, Piscataway, NJ 08854, USA
              Tel: 732 445 3801
              Fax: 732 445 5735
              Email: bharti@waksman.rutgers.edu
              Seq primer: T7
              Class: BAC ends
              High quality sequence start: 79.
Location/Qualifiers
source
  1..936
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  /mol_type="genomic DNA"
  /cultivar="B73"
  /sub_species="mays"
  /db_xref="taxon:4578"
  /clone="ZMMBBC0024C16"
  /lab_host="E. coli DH10B"
  /clone_lib="ZMMBBC (ECORI)"
  /note="Vector: pTARBAC2.1; Site_1: EcorI; Site_2: EcorI"
ORIGIN
Query Match      27.8%; Score 35.8; DB 29; Length 936;

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Best Local Similarity 63.2%; Pred. No. 3 4;
Matches 55; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 4 TTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTCGTGTA 63
Db 649 TTAATAAAATAGTTTCATGATTTTAGGTTAAATAAGGAATTTTAAGGCATTAAAGTA 708

QY 64 GTGAATAGAGTTAGGCAGGATATTC 90
Db 709 GTTAAAGTGTAGTTATGATTTT 735

RESULT 7
CG019434/c
LOCUS ZUAFN74TH ZM 3.0 4.0 KB Zea mays genomic clone ZMMBPa0052N04,
DEFINITION genomic survey sequence.
ACCESSION CG019434
VERSION CG019434.1 GI:33891599
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 270)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
Citek.R.W., Nurnberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSSs: ZUAFN74TV
Contact: Cathy Whitelaw
TICK 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
Location/Qualifiers
1..270
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBPa0052N04"
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/note="Vector: pBCSK-; Site 1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"
ORIGIN
Query Match 26.5%; Score 34.2; DB 29; Length 270;
Best Local Similarity 62.1%; Pred. No. 8.6;
Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 TTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTCGTGTA 63
Db 248 TTAATAAAATAGTTTTCATGATTTTAGGTTAAATAAGGAATTTTAAGGCATTAAAGTA 189

QY 64 GTGAATAGAGTTAGGCAGGATATTC 90
Db 188 GTTAAAGTGTAGTTATGATTTT 162

RESULT 8
CC167485
LOCUS CC167485
DEFINITION ik30c12.g2 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
ik30c12, genomic survey sequence.
ACCESSION CC167485
VERSION CC167485.1 GI:30199003
KEYWORDS GSS.

Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 782)
AUTHORS Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: ik30 row: c column: 12
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 782.
FEATURES
Location/Qualifiers
1..782
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ik30c12"
/lab_host="DH5a"
/clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: Immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (.X/y
reads in M13mp19, b/g reads in pUC19). The same ligation
was transformed into DH5a."
ORIGIN
Query Match 26.5%; Score 34.2; DB 28; Length 782;
Best Local Similarity 62.1%; Pred. No. 9.9;
Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 TTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTCGTGTA 63
Db 540 TTAATAAAATAGTTGATGATTTTAGGTTAAATAAGGAATTTTAAGGCATTAAAGTA 599

QY 64 GTGAATAGAGTTAGGCAGGATATTC 90
Db 600 GTTAAAGTGTAGTTCTGGATTTT 626

RESULT 9
BH332797
LOCUS BH332797
DEFINITION CH230-5917.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-5917, genomic survey sequence.
ACCESSION BH332797
VERSION BH332797.1 GI:17263511
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 794)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Teegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,P., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)

```



```

COMMENT
Other GSSs: CH230-5917.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tc/bac_ends/rat/bac_end_intro.html
Plate: 59 row: I column: 7
Seq primer: SP6
Class: BAC ends.

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                /cell_type="Brain"
                /clone_lib="CHORI-230 Segment 1"
                /note="vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
                CHORI-230 Rat (BN/SENHsd/MCW) BAC library produced by
                Pieter de Jong"

ORIGIN
Query Match      26.5%; Score 34.2; DB 28; Length 794;
Best Local Similarity 62.1%; Pred. No. 10;
Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 8 TAATGATAGTAGGAGGCTTGTAGTTTAAAGAPAGTTTTCGTGCTTCTGTAGTGA 67
Db 532 TTATTATAGTAGGAATCTAGGCGAGGAGAGAGTGGTTCCTCTCTTATGTGCTTA 591

QY 68 ATAGAGTTAGGACGGGATATTCACAT 94
Db 592 ACACGGTATTGCTAGTACAGTCACAT 618

RESULT 10
CC986340/c
LOCUS
DEFINITION
ZUAFM74TH ZM 3.0 4.0 KB Zea mays genomic clone ZMMBPa0052N03,
genomic survey sequence.
ACCESSION
CC986340
VERSION
CC986340.1 GI:33846216
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 805)
Whitealaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: ZUAFM74TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
    source
        Location/Qualifiers
            1..805
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                /clone_lib="ZM 3.0 4.0 KB"
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                genomic DNA library"

ORIGIN
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Best Local Similarity 62.1%; Pred. No. 10;
Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 TTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTCGTGCTTCTGTA 63
Db 248 TTAATAAAAATAGTTTGTGATTTTAGGTTAAATAAGGAATTTTAAGGCATTTTAAGTA 189

QY 64 GTCAATAGAGTTAGGCGAGGATATTC 90
Db 188 GTTAAAGATATTAGTTATGGAATTTTA 162

RESULT 11
CC670625
LOCUS
DEFINITION
OGWB724TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0531C24,
genomic survey sequence.
ACCESSION
CC670625
VERSION
CC670625.1 GI:32074895
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 807)
Whitealaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGWB724TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
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ORIGIN
Query Match      26.5%; Score 34.2; DB 29; Length 807;
Best Local Similarity 62.1%; Pred. No. 10;
Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 TTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAAGATAGTTTTCGTGCTTCTGTA 63
Db 660 TTAATAAAAATAGTTTTCATGGTTTTAGGTTAAATAAGGAATTTTAAGGTATTAAAGTA 719

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QY 64 GTCAATAGAGTTAGGAGGAGGATTTCA 90
 Db 720 GTTAAAGCATTAGTCTGGATTTTA 746

RESULT 12
 CG464137/c
 LOCUS
 DEFINITION ZUHN35TV ZM 3.0 4.0 KB Zea mays genomic clone ZMMPa0070F22,
 genomic survey sequence.
 ACCESSION CG464137
 VERSION CG464137.1 GI:34849137
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 935)
 AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
 Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics
 Unpublished (2002)
 JOURNAL Other GSSs: ZUHN35TH
 COMMENT Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TF
 Class: sheared ends.

FEATURES
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 1..935
 /organism="Zea mays"
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 /note="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'
 genomic DNA library"

ORIGIN
 Query Match 26.5%; Score 34.2; DB 29; Length 935;
 Best Local Similarity 62.1%; Pred. No. 10;
 Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 4 TTCATAATGATAGTAGGAGGCTTGTAGGTTTAAAGATAGTTTGTCTACTTTCTGTA 63
 Db 348 TTAATAAATAATAGTTTGTGATTTTAGGTTAAATAGGAATTTAAGGCATTTTAAGTA 289

QY 64 GTCAATAGAGTTAGGAGGAGGATTTCA 90
 Db 288 GTTAAAGTATTAGTTATGATTTTA 262

RESULT 13
 BQ098469
 LOCUS
 DEFINITION Phl8c07.y2 Ostertagia ostertagi L3 pAMP1 v1 Ostertagia ostertagi
 cDNA 5' similar to SW:GCHI.OSTOS 061573 GTP CYCLOHYDROLASE I
 ;contains Alu repetitive element;; mRNA sequence.
 ACCESSION BQ098469
 VERSION BQ098469.1 GI:20131446
 KEYWORDS EST.
 SOURCE Ostertagia ostertagi
 ORGANISM Ostertagia ostertagi
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 Trichostrongyloidea; Haemonchidae; Ostertaginae; Ostertagia.
 REFERENCE 1 (bases 1 to 513)
 AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,

Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
 Bowers,F., Gibbons,M., Ritter,B., Bennett,J., Franklin,C.,
 Tsagarisvili,R., Ronko,I., Kennedy,S., McGuire,L., Beck,C.,
 Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
 McCann,R., Waterston,R. and Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 CONTACT: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter
 at Washington University, St. Louis. DNA Sequencing by: Washington
 University Genome Sequencing Center
 High quality sequence stop: 418.

FEATURES
 source
 1..513
 /organism="Ostertagia ostertagi"
 /mol_type="mRNA"
 /db_xref="taxon:6317"
 /dev_stage="L3"
 /lab_host="DH10B"
 /clone_lib="Ostertagia ostertagi L3 pAMP1 v1"
 /note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
 ***WARNING: Subsequent examination of these samples has
 revealed the presence of an additional Trichostrongyloidea
 cattle nematode, Cooperia oncophora. Sequences in this
 library may derive from either Ostertagia or Cooperia.***
 The library was constructed by Claire Murphy and Dr. James
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 Gasbarre of the USDA, Beltsville, MD
 (lgasbarre@nri.barc.usda.gov). Third stage exsheathed
 larvae were collected from 14 day fecal-sphagnum moss
 cultures of Ostertagia eggs. The larvae were recovered by
 overnight passage on a Baermann apparatus, and then
 cleaned by passage through a 20 micron nylon mesh. The
 larvae were then subjected to a treatment with 1.25%
 chlorox to induce excystation. The larvae were washed with
 5 changes of PBS, and then pelleted and snap frozen in
 liquid nitrogen."

ORIGIN
 Query Match 25.9%; Score 33.4; DB 13; Length 513;
 Best Local Similarity 62.7%; Pred. No. 16;
 Matches 52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 37 AGAATAGTTTGTCTGTTCTTCTGTAGTGAATAGTACGAGGATATTCACCTTA 96
 Db 430 AGAAGATTCTTGAATCTCATTCAAGTGAAGTAACTAGTACGATTCACGAGTA 489

QY 97 TCGTTTCAGACCCACCTCCCAAT 119
 Db 490 TTTTTCGACACAAATGACAAAT 512

RESULT 14
 BQ099257
 LOCUS
 DEFINITION BQ099257
 ;contains Alu repetitive element;; mRNA sequence.
 ACCESSION BQ099257
 VERSION BQ099257.1 GI:20132241
 KEYWORDS EST.
 SOURCE Ostertagia ostertagi

ORGANISM Ostertagia ostertagi
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Ostertaginae; Ostertagia.

REFERENCE 1 (bases 1 to 535)
AUTHORS McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagarisvili, R., Ronko, I., Kennedy, S., McGuire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)

TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter
at Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center
High quality sequence stop: 419.

FEATURES source
1..535
/organism="Ostertagia ostertagi"
/mol_type="mRNA"
/db_xref="taxon:6317"
/dev_stage="L3"
/lab_host="DH10B"
/clone_lib="Ostertagia ostertagi L3 pAMP1 v1"
/notes="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
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QY 37 AGAATAGTTTTGCTGTTACTTTCTGTAGTGAATAGAGTTAGCGAGGATATTCACCAATTA 96
|||||
Db 430 AGAAGAAATCTTGTGAATCTCATTCAAGTGAATGAGTAACTAGTACGAGTATTCACGAGTA 489
|||||
QY 97 TCGTTTCAGACCCACCTCCCAAT 119
|||||
Db 490 TTTTTCGACACAAATGACAAT 512
|||||

RESULT 15
BQ099653 536 bp mRNA linear EST 20-DEC-2002
LOCUS ph33a09.y2 Ostertagia ostertagi L3 pAMP1 v1 Ostertagia ostertagi
DEFINITION cDNA 5' similar to SW:GCH1_OSTOS 061573 GTP CYCLOHYDROLASE 1

; contains Alu repetitive element, mRNA sequence.

ACCESSION BQ099653
VERSION BQ099653.1 GI:20132637
KEYWORDS EST
SOURCE Ostertagia ostertagi
ORGANISM Ostertagia ostertagi
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Ostertaginae; Ostertagia.

REFERENCE 1 (bases 1 to 535)
AUTHORS McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
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Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagarisvili, R., Ronko, I., Kennedy, S., McGuire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
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Unpublished (1999)

TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
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Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter
at Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center
High quality sequence stop: 425.

FEATURES source
1..536
/organism="Ostertagia ostertagi"
/mol_type="mRNA"
/db_xref="taxon:6317"
/dev_stage="L3"
/lab_host="DH10B"
/clone_lib="Ostertagia ostertagi L3 pAMP1 v1"
/notes="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
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QY 37 AGAATAGTTTTGCTGTTACTTTCTGTAGTGAATAGAGTTAGCGAGGATATTCACCAATTA 96
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|||||
Db 491 TTTTTCGACACAAATGACAAT 513
|||||

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